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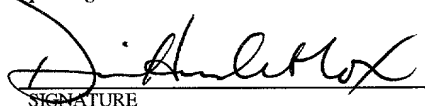
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FORM PTO-1390 OFFICE		U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK	ATTORNEY'S DOCKET NUMBER PF-0721 USN
TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371			U.S. APPLICATION NO. (If known, use 37 CFR 1.51 TO BE ASSIGNED) 10/031905
INTERNATIONAL APPLICATION NO. PCT/US00/19980	INTERNATIONAL FILING DATE 20 July 2000	PRIORITY DATE CLAIMED 22 July 1999	
TITLE OF INVENTION HUMAN SYNTHETASES			
APPLICANT(S) FOR DO/EO/US TANG, Y. Tom; YUE, HILLMAN, Jennifer L.; BANDMAN, Olga; YUE, Henry; BAUGHN, Mariah R.; LAL, Preeti; LU, Dyung, Aina M.; SHAH, Purvi; AZIMZAI, Yalda			
<p>Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:</p> <ol style="list-style-type: none"> <input checked="" type="checkbox"/> This is the FIRST submission of items concerning a filing under 35 U.S.C. 371. <input type="checkbox"/> This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371. <input type="checkbox"/> This is an express request to promptly begin national examination procedures (35 U.S.C. 371 (f)). <input type="checkbox"/> The US has been elected by the expiration of 19 months from the priority date (PCT Article 31). <input checked="" type="checkbox"/> A copy of the International Application as filed (35 U.S.C. 371(c)(2)) <ol style="list-style-type: none"> <input type="checkbox"/> is attached hereto (required only if not communicated by the International Bureau) <input type="checkbox"/> has been communicated by the International Bureau. <input checked="" type="checkbox"/> is not required, as the application was filed in the United States Receiving Office (RO/US). <input type="checkbox"/> An English language translation of the International Application as filed (35 U.S.C. 371(c)(2)). <input checked="" type="checkbox"/> Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3)) <ol style="list-style-type: none"> <input type="checkbox"/> are attached hereto (required only if not communicated by the International Bureau). <input type="checkbox"/> have been communicated by the International Bureau. <input type="checkbox"/> have not been made; however, the time limit for making such amendments has NOT expired. <input type="checkbox"/> have not been made and will not be made. <input checked="" type="checkbox"/> attached hereto Article 34 Amendment <input type="checkbox"/> An English language translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)). <input checked="" type="checkbox"/> An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)). <input type="checkbox"/> An English language translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)). <p>Items 11 to 16 below concern document(s) or information included:</p> <ol style="list-style-type: none"> <input type="checkbox"/> An Information Disclosure Statement under 37 CFR 1.97 and 1.98. <input checked="" type="checkbox"/> An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.27 and 3.31 is included. <input checked="" type="checkbox"/> A FIRST preliminary amendment, as follows: Cancel in this application original claims #12, 14, 18, 20, 21, 23 24, 27 before calculating the filing fee, without prejudice or disclaimer. Applicants submit that these claims were included in the application as filed in the interest of providing notice to the public of certain specific subject matter intended to be claimed, and are being canceled at this time in the interest of reducing filing costs. Applicants expressly state that these claims are not being canceled for reasons related to patentability, and are in fact fully supported by the specification as filed. Applicants expressly reserve the right to reinstate these claims or to add other claims during prosecution of this application or a continuation or divisional application. Applicants expressly do not disclaim the subject matter of any invention disclosed herein which is not set forth in the instantly filed claims. <input type="checkbox"/> A SECOND or SUBSEQUENT preliminary amendment. <input type="checkbox"/> A substitute specification <input type="checkbox"/> A change of power of attorney and/or address letter. <input checked="" type="checkbox"/> Other items or information: <ol style="list-style-type: none"> Transmittal Letter (2 pp, in duplicate) Return Postcard Express Mail Label No.: EL 856149101 US Sequence Listing Statement, and Sequence Listing Diskette Article 34 Amendment 			

U.S. APPLICATION NO. (if known, see 37 CFR 1.5) 10/031905 TO BE ASSIGNED	INTERNATIONAL APPLICATION NO.: PCT/US00/19980	ATTORNEY'S DOCKET NUMBER PF-0721 USN																																																						
17. <input checked="" type="checkbox"/> The following fees are submitted: BASIC NATIONAL FEE (37 CFR 1.492(a)(1)-(5)): Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO.\$1000.00 <input type="checkbox"/> International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO..\$860.00 International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.445(a)(2)) paid to USPTO.....\$710.00 <input checked="" type="checkbox"/> International preliminary examination fee paid to USPTO (37 CFR 1.482) but all claims did not satisfy provisions of PCT Article 33(1)-(4).....\$690.00 <input type="checkbox"/> International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(1)-(4).....\$100.00																																																								
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<table border="1" style="width: 100%; border-collapse: collapse;"> <tr> <th style="width: 20%;">CLAIMS</th> <th style="width: 20%;">NUMBER FILED</th> <th style="width: 20%;">NUMBER EXTRA</th> <th style="width: 40%;">RATE</th> </tr> <tr> <td>Total Claims</td> <td style="text-align: center;">20 =</td> <td style="text-align: center;">0</td> <td style="text-align: center;">X \$ 18.00</td> </tr> <tr> <td>Independent Claims</td> <td style="text-align: center;">3 =</td> <td style="text-align: center;">0</td> <td style="text-align: center;">X \$ 80.00</td> </tr> <tr> <td colspan="3" style="padding-top: 5px;">MULTIPLE DEPENDENT CLAIM(S) (if applicable)</td> <td style="text-align: center; padding-top: 5px;">+ \$270.00</td> </tr> <tr> <td colspan="3" style="text-align: right; padding-top: 5px;">TOTAL OF ABOVE CALCULATIONS =</td> <td style="text-align: center; padding-top: 5px;">\$</td> </tr> <tr> <td colspan="3" style="padding: 5px;"> <input type="checkbox"/> Applicant claims small entity status. See 37 CFR 1.27. The fees indicated above are reduced by 1/2. </td> <td style="text-align: center; padding: 5px;"> \$ </td> </tr> <tr> <td colspan="3" style="text-align: right; padding-top: 5px;">SUBTOTAL</td> <td style="text-align: center; padding-top: 5px;">\$710.00</td> </tr> <tr> <td colspan="3" style="text-align: right; padding-top: 5px;">=</td> <td></td> </tr> <tr> <td colspan="3" style="padding: 5px;"> Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(f)). </td> <td style="text-align: center; padding: 5px;"> \$ </td> </tr> <tr> <td colspan="3" style="text-align: right; padding-top: 5px;">TOTAL NATIONAL FEE =</td> <td style="text-align: center; padding-top: 5px;">\$710.00</td> </tr> <tr> <td colspan="3" style="padding: 5px;"> Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by the appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property </td> <td style="text-align: center; padding: 5px;"> \$ </td> </tr> <tr> <td colspan="3" style="text-align: right; padding-top: 5px;">TOTAL FEES ENCLOSED =</td> <td style="text-align: center; padding-top: 5px;">\$710.00</td> </tr> <tr> <td colspan="2" style="padding: 5px;"></td> <td style="text-align: center; padding: 5px;"> Amount to be Refunded: </td> <td style="text-align: center; padding: 5px;"> \$ </td> </tr> <tr> <td colspan="2" style="padding: 5px;"></td> <td style="text-align: center; padding: 5px;"> Charged </td> <td style="text-align: center; padding: 5px;"> \$ </td> </tr> </table>	CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE	Total Claims	20 =	0	X \$ 18.00	Independent Claims	3 =	0	X \$ 80.00	MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$270.00	TOTAL OF ABOVE CALCULATIONS =			\$	<input type="checkbox"/> Applicant claims small entity status. See 37 CFR 1.27. The fees indicated above are reduced by 1/2.			\$	SUBTOTAL			\$710.00	=				Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(f)).			\$	TOTAL NATIONAL FEE =			\$710.00	Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by the appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property			\$	TOTAL FEES ENCLOSED =			\$710.00			Amount to be Refunded:	\$			Charged	\$
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a. <input type="checkbox"/> A check in the amount of \$ _____ to cover the above fees is enclosed. b. <input checked="" type="checkbox"/> Please charge my Deposit Account No. <u>09-0108</u> in the amount of <u>\$710.00</u> to cover the above fees. c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>09-0108</u> . A duplicate copy of this sheet is enclosed. NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status. SEND ALL CORRESPONDENCE TO: INCYTE GENOMICS, INC 3160 Porter Drive Palo Alto, CA 94304 <div style="text-align: center;">  SIGNATURE NAME: Diana Hamlet-Cox REGISTRATION NUMBER: 33,302 DATE: <u>18 January 2002</u> </div>																																																								

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PTO/PCT Rec'd 18 JAN 2002
HUMAN SYNTHETASES

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TECHNICAL FIELD

This invention relates to nucleic acid and amino acid sequences of synthetases and to the use of these sequences in the diagnosis, treatment, and prevention of immune, neuronal, and reproductive disorders, and cell proliferative disorders including cancer.

10

BACKGROUND OF THE INVENTION

A large number of cellular biosynthetic intermediary metabolism processes involve intermolecular transfer of carbon atom-containing substrates (carbon substrates). Examples of such reactions include the tricarboxylic acid cycle, synthesis of fatty acids and long-chain phospholipids, synthesis of alcohols and aldehydes, synthesis of intermediary metabolites, and reactions involved in the amino acid degradation pathways. Many of these reactions are catalyzed by synthetases (also called ligases), which catalyze the formation of a bond between two substrate molecules. Some of these reactions require input of energy, usually in the form of conversion of ATP to either ADP or AMP and pyrophosphate. Synthetases are named for the products of the reaction they catalyze and are involved in such processes as metabolism and the synthesis of macromolecules.

15
20 Ligases forming carbon-oxygen bonds

Proteins make up more than half of the total dry mass of a cell. The synthesis of proteins is central to cell maintenance, growth, and development. Synthesis occurs on ribosomes and depends on the cooperative interaction of several classes of RNA molecules. The process begins with transcription of the genetic code contained within the DNA to form messenger RNA (mRNA). The mRNA moves in steps through a ribosome and the nucleotide sequence of the mRNA is translated into a corresponding sequence of amino acids to construct a distinct protein chain.

The aminoacyl-transfer RNA (tRNA) synthetases are important RNA-associated enzymes with roles in translation. Protein biosynthesis depends on each amino acid forming a linkage with the appropriate tRNA. The aminoacyl-tRNA synthetases are responsible for the activation and correct attachment of an amino acid with its cognate tRNA. The 20 aminoacyl-tRNA synthetase enzymes can be divided into two structural classes, and each class is characterized by a distinctive topology of the catalytic domain. Class I enzymes contain a catalytic domain based on the nucleotide-binding Rossman 'fold'. Class II enzymes contain a central catalytic domain, which consists of a seven-stranded antiparallel β -sheet motif, as well as N- and C- terminal regulatory domains. Class II enzymes are separated into two groups based on the heterodimeric or homodimeric structure of the enzyme; the latter group is further subdivided by the structure of the N- and C-terminal regulatory

domains (Hartlein, M. and Cusack, S. (1995) J. Mol. Evol. 40:519-530). Autoantibodies against aminoacyl-tRNAs are generated by patients with dermatomyositis and polymyositis, and correlate strongly with complicating interstitial lung disease (ILD). These antibodies appear to be generated in response to viral infection, and coxsackie virus has been used to induce experimental viral myositis in animals (Friedman, A.W. et al. (1996) Semin. Arthritis Rheum. 26:459-467). A synthetase homolog has been shown to be expressed in chronic myeloid leukemia (CML). A phenylalanine-tRNA synthetase homolog has been found to be tumor-selective and expressed in a cell cycle stage- and differentiation-dependent fashion in an acute-phase human CML cell line (Sen, S. et al. (1997) Proc. Natl. Acad. Sci. USA 94:6164-6169).

10 Ligases forming carbon-sulfur bonds (Acid-thiol ligases)

In many cases, a carbon substrate is derived from a small molecule containing at least two carbon atoms. The carbon substrate is often covalently bound to a larger molecule which acts as a carbon substrate carrier molecule within the cell. In the biosynthetic mechanisms described above, the carrier molecule is coenzyme A. Coenzyme A (CoA) is structurally related to derivatives of the nucleotide ADP and consists of 4'-phosphopantetheine linked via a phosphodiester bond to the alpha phosphate group of adenosine 3',5'-bisphosphate. The terminal thiol group of 4'-phosphopantetheine acts as the site for carbon substrate bond formation. The predominant carbon substrates which utilize CoA as a carrier molecule during biosynthesis and intermediary metabolism in the cell are acetyl, succinyl, and propionyl moieties, collectively referred to as acyl groups. Other carbon substrates include enoyl lipid, which acts as a fatty acid oxidation intermediate, and carnitine, which acts as an acetyl-CoA flux regulator/ mitochondrial acyl group transfer protein. Acyl-CoA and acetyl-CoA are synthesized in the cell by acyl-CoA synthetase and acetyl-CoA synthetase, respectively.

Activation of fatty acids is mediated by at least three forms of acyl-CoA synthetase activity:

- i) acetyl-CoA synthetase, which activates acetate and several other low molecular weight carboxylic acids and is found in muscle mitochondria and the cytosol of other tissues; ii) medium-chain acyl-CoA synthetase, which activates fatty acids containing between four and eleven carbon atoms (predominantly from dietary sources), and is present only in liver mitochondria; and iii) acyl CoA synthetase, which is specific for long chain fatty acids with between six and twenty carbon atoms, and is found in microsomes and the mitochondria. Proteins associated with acyl-CoA synthetase activity have been identified from many sources including bacteria, yeast, plants, mouse, and man. The activity of acyl-CoA synthetase may be modulated by phosphorylation of the enzyme by cAMP-dependent protein kinase. The COL4A5 (collagen, type IV, alpha-5) chromosomal region found deleted in 2 patients with Alport syndrome, elliptocytosis, and mental retardation (Piccini, M. et al. (1998) Genomics 47: 350-358) is contiguous with the region containing long-chain acyl-CoA synthetase 4 (FACL4). Therefore, it has been suggested (Piccini supra) that the absence of FACL4 may be involved in the development of mental retardation and other phenotypes associated with

Alport syndrome in these patients.

Ligases forming carbon-nitrogen bonds

A key representative of the amide synthases is the enzyme glutamine synthetase (glutamate-ammonia ligase) that catalyzes the amination of glutamic acid to glutamine by ammonia using the energy of ATP hydrolysis. Glutamine is the primary source for the amino group in various amide transfer reactions involved in de novo pyrimidine nucleotide synthesis and in purine and pyrimidine ribonucleotide interconversions, as well as the conversion of aspartate to asparagine. Overexpression of glutamine synthetase has been observed in primary liver cancer (Christa, L. et al. (1994) Gastroent. 106:1312-1320).

Cyclo-ligases and other carbon-nitrogen ligases comprise various enzymes and enzyme complexes that participate in the de novo pathways to purine and pyrimidine biosynthesis. Because these pathways are critical to the synthesis of nucleotides for replication of both RNA and DNA, many of these enzymes have been the targets of clinical agents for the treatment of cell proliferative disorders such as cancer and infectious diseases.

Purine biosynthesis occurs de novo from the amino acids glycine and glutamine, and other small molecules. Three of the key reactions in this process are catalyzed by a trifunctional enzyme composed of glycinamide-ribonucleotide synthetase (GARS), aminoimidazole ribonucleotide synthetase (AIRS), and glycinamide ribonucleotide transformylase (GART). Together these three enzymes combine ribosylamine phosphate with glycine to yield phosphoribosyl aminoimidazole, a precursor to both adenylate and guanylate nucleotides. This trifunctional protein has been implicated in the pathology of Downs syndrome (Aimi, J. et al. (1990) Nucleic Acid Res. 18:6665-6672). Adenylosuccinate synthetase catalyzes a later step in purine biosynthesis that converts inosinic acid to adenylosuccinate, a key step on the path to ATP synthesis. This enzyme is also similar to another carbon-nitrogen ligase, argininosuccinate synthetase, that catalyzes a similar reaction in the urea cycle (Powell, S.M. et al. (1992) FEBS Lett. 303:4-10).

Like the de novo biosynthesis of purines, de novo synthesis of the pyrimidine nucleotides uridylate and cytidylate also arises from a common precursor, in this instance the nucleotide orotidylate derived from orotate and phosphoribosyl pyrophosphate (PPRP). Again a trifunctional enzyme comprising three carbon-nitrogen ligases plays a key role in the process. In this case the enzymes aspartate transcarbamylase (ATCase), carbamyl phosphate synthetase II, and dihydroorotase (DHOase) are encoded by a single gene called CAD. Together these three enzymes combine the initial reactants in pyrimidine biosynthesis, glutamine, CO₂ and ATP to form dihydroorotate, the precursor to orotate and orotidylate (Iwahana, H. et al. (1996) Biochem. Biophys. Res. Commun. 219:249-255). Further steps then lead to the synthesis of uridine nucleotides from orotidylate. Cytidine nucleotides are derived from uridine-5'-triphosphate (UTP) by the amidation of UTP using glutamine as the amino donor and the enzyme CTP synthetase. Regulatory mutations in the human

CTP synthetase are believed to confer multi-drug resistance to agents widely used in cancer therapy (Yamauchi, M. et al. (1990) EMBO J. 9:2095-2099).

Ligases forming carbon-carbon bonds

Ligases in this group are represented by the carboxylases acetyl-CoA carboxylase and pyruvate carboxylase. Acetyl-CoA carboxylase is a complex which includes a biotin carboxyl carrier protein, biotin carboxylase, and a carboxyl transferase made up of two alpha and two beta subunits. This complex catalyzes the carboxylation of Acetyl-CoA from CO₂ and H₂O using the energy of ATP hydrolysis (PRINTS document PR01069). Acetyl-CoA carboxylase is the rate-limiting step in the biogenesis of long-chain fatty acids. Two isoforms of Acetyl-CoA carboxylase, types I and types II, are expressed in humans in a tissue-specific manner (Ha, J. et al. (1994) Eur. J. Biochem. 219:297-306). Pyruvate carboxylase is a nuclear-encoded mitochondrial enzyme that catalyzes the conversion of pyruvate to oxaloacetate, a key intermediate in the citric acid cycle.

Ligases forming phosphoric ester bonds

Ligases in this group are represented by the DNA ligases involved in both DNA replication and repair. DNA ligases seal phosphodiester bonds between two adjacent nucleotides in a DNA chain using the energy from ATP hydrolysis to first activate the free 5'-phosphate of one nucleotide and then react it with the 3'-OH group of the adjacent nucleotide. This resealing reaction is used in both DNA replication to join small DNA fragments called "Okazaki" fragments that are transiently formed in the process of replicating new DNA, and in DNA repair. DNA repair is the process by which accidental base changes, such as those produced by oxidative damage, hydrolytic attack, or uncontrolled methylation of DNA, are corrected before replication or transcription of the DNA can occur. Bloom's syndrome is an inherited human disease in which individuals are partially deficient in DNA ligation and consequently have an increased incidence of cancer (Alberts, B. et al. (1994) The Molecular Biology of the Cell, Garland Publishing Inc., New York, NY, p. 247).

The discovery of new synthetases and the polynucleotides encoding them satisfies a need in the art by providing new compositions which are useful in the diagnosis, prevention, and treatment of immune, neuronal, and reproductive disorders, and cell proliferative disorders including cancer.

SUMMARY OF THE INVENTION

The invention features purified polypeptides, human synthetases, referred to collectively as "SYNT" and individually as "SYNT-1," "SYNT-2," "SYNT-3," "SYNT-4," "SYNT-5," "SYNT-6," "SYNT-7," "SYNT-8," "SYNT-9," "SYNT-10," "SYNT-11," "SYNT-12," "SYNT-13," "SYNT-14," and "SYNT-15." In one aspect, the invention provides an isolated polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID

NO:1-15, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-15. In one alternative, the invention provides an isolated polypeptide comprising the amino acid sequence of SEQ ID NO:1-15.

5 The invention further provides an isolated polynucleotide encoding a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, c) a biologically active fragment of an amino acid sequence selected from the group
10 consisting of SEQ ID NO:1-15, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-15. In one alternative, the polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NO:1-15. In another alternative, the polynucleotide is selected from the group consisting of SEQ ID NO:16-30.

Additionally, the invention provides a recombinant polynucleotide comprising a promoter
15 sequence operably linked to a polynucleotide encoding a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, c) a biologically active fragment of an amino acid sequence selected from the group consisting of
20 SEQ ID NO:1-15, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-15. In one alternative, the invention provides a cell transformed with the recombinant polynucleotide. In another alternative, the invention provides a transgenic organism comprising the recombinant polynucleotide.

The invention also provides a method for producing a polypeptide comprising an amino acid
25 sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, and d) an immunogenic fragment of an amino acid sequence selected from the
30 group consisting of SEQ ID NO:1-15. The method comprises a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding the polypeptide, and b) recovering the polypeptide so expressed.

Additionally, the invention provides an isolated antibody which specifically binds to a
35 polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, b) a naturally occurring amino

acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-15.

- 5 The invention further provides an isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:16-30, b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:16-30, c) a polynucleotide sequence complementary to a), d) a polynucleotide sequence
10 complementary to b), and e) an RNA equivalent of a)-d). In one alternative, the polynucleotide comprises at least 60 contiguous nucleotides.

- Additionally, the invention provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group
15 consisting of SEQ ID NO:16-30, b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:16-30, c) a polynucleotide sequence complementary to a), d) a polynucleotide sequence complementary to b), and e) an RNA equivalent of a)-d). The method comprises a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence
20 complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and b) detecting the presence or absence of said hybridization complex, and optionally, if present, the amount thereof. In one alternative, the probe comprises at least 60 contiguous nucleotides.

- 25 The invention further provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:16-30, b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID
30 NO:16-30, c) a polynucleotide sequence complementary to a), d) a polynucleotide sequence complementary to b), and e) an RNA equivalent of a)-d). The method comprises a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

- 35 The invention further provides a pharmaceutical composition comprising an effective amount of a polypeptide comprising an amino acid sequence selected from the group consisting of a) an

amino acid sequence selected from the group consisting of SEQ ID NO:1-15, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, and a pharmaceutically acceptable excipient. In one embodiment, the pharmaceutical composition comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1-15. The invention additionally provides a method of treating a disease or condition associated with decreased expression of functional SYNT, comprising administering to a patient in need of such treatment the pharmaceutical composition.

The invention also provides a method for screening a compound for effectiveness as an agonist of a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-15. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. In one alternative, the invention provides a pharmaceutical composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with decreased expression of functional SYNT, comprising administering to a patient in need of such treatment the pharmaceutical composition.

Additionally, the invention provides a method for screening a compound for effectiveness as an antagonist of a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-15. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample. In one alternative, the invention provides a pharmaceutical composition comprising an antagonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with overexpression of functional SYNT, comprising administering to a patient in need of such treatment the pharmaceutical composition.

The invention further provides a method of screening for a compound that specifically binds to a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-15. The method comprises a) combining the polypeptide with at least one test compound under suitable conditions, and b) detecting binding of the polypeptide to the test compound, thereby identifying a compound that specifically binds to the polypeptide.

The invention further provides a method of screening for a compound that modulates the activity of a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-15, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-15. The method comprises a) combining the polypeptide with at least one test compound under conditions permissive for the activity of the polypeptide, b) assessing the activity of the polypeptide in the presence of the test compound, and c) comparing the activity of the polypeptide in the presence of the test compound with the activity of the polypeptide in the absence of the test compound, wherein a change in the activity of the polypeptide in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide.

The invention further provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence selected from the group consisting of SEQ ID NO:16-30, the method comprising a) exposing a sample comprising the target polynucleotide to a compound, and b) detecting altered expression of the target polynucleotide.

The invention further provides a method for assessing toxicity of a test compound, said method comprising a) treating a biological sample containing nucleic acids with the test compound; b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide comprising a polynucleotide sequence selected from the group consisting of i) a polynucleotide sequence selected from the group consisting of SEQ ID NO:16-30, ii) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:16-30, iii) a polynucleotide sequence complementary to i), iv) a polynucleotide sequence complementary to ii),

and v) an RNA equivalent of i)-iv). Hybridization occurs under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:16-30, ii) a naturally occurring polynucleotide sequence having at least 5 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:16-30, iii) a polynucleotide sequence complementary to i), iv) a polynucleotide sequence complementary to ii), and v) an RNA equivalent of i)-iv). Alternatively, the target polynucleotide comprises a fragment of the above polynucleotide sequence; c) quantifying the amount of hybridization complex; and d) comparing the amount of hybridization complex in the treated 10 biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

BRIEF DESCRIPTION OF THE TABLES

15 Table 1 shows polypeptide and nucleotide sequence identification numbers (SEQ ID NOs), clone identification numbers (clone IDs), cDNA libraries, and cDNA fragments used to assemble full-length sequences encoding SYNT.

Table 2 shows features of each polypeptide sequence, including potential motifs, homologous sequences, and methods, algorithms, and searchable databases used for analysis of SYNT.

20 Table 3 shows selected fragments of each nucleic acid sequence; the tissue-specific expression patterns of each nucleic acid sequence as determined by northern analysis; diseases, disorders, or conditions associated with these tissues; and the vector into which each cDNA was cloned.

Table 4 describes the tissues used to construct the cDNA libraries from which cDNA clones 25 encoding SYNT were isolated.

Table 5 shows the tools, programs, and algorithms used to analyze the polynucleotides and polypeptides of the invention, along with applicable descriptions, references, and threshold parameters.

DESCRIPTION OF THE INVENTION

30 Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular machines, materials and methods described, as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which 35 will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an,"

and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a host cell" includes a plurality of such host cells, and a reference to "an antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

5 Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any machines, materials, and methods similar or equivalent to those described herein can be used to practice or test the present invention, the preferred machines, materials and methods are now described. All publications mentioned herein are cited for the purpose of describing and disclosing
10 the cell lines, protocols, reagents and vectors which are reported in the publications and which might be used in connection with the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

"SYNT" refers to the amino acid sequences of substantially purified SYNT obtained from
15 any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and human, and from any source, whether natural, synthetic, semi-synthetic, or recombinant.

The term "agonist" refers to a molecule which intensifies or mimics the biological activity of SYNT. Agonists may include proteins, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of SYNT either by directly interacting with
20 SYNT or by acting on components of the biological pathway in which SYNT participates.

An "allelic variant" is an alternative form of the gene encoding SYNT. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. A gene may have none, one, or many allelic variants of its naturally occurring form. Common mutational changes which give rise to
25 allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

"Altered" nucleic acid sequences encoding SYNT include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as SYNT or a
30 polypeptide with at least one functional characteristic of SYNT. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding SYNT, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding SYNT. The encoded protein may also be "altered," and may contain deletions, insertions, or
35 substitutions of amino acid residues which produce a silent change and result in a functionally equivalent SYNT. Deliberate amino acid substitutions may be made on the basis of similarity in

polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of SYNT is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, and positively charged amino acids may include lysine and arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine. Amino acids with uncharged side chains having similar hydrophilicity values may include: leucine, isoleucine, and valine; glycine and alanine; and phenylalanine and tyrosine.

The terms "amino acid" and "amino acid sequence" refer to an oligopeptide, peptide, polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring or synthetic molecules. Where "amino acid sequence" is recited to refer to a sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

"Amplification" relates to the production of additional copies of a nucleic acid sequence. Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art.

The term "antagonist" refers to a molecule which inhibits or attenuates the biological activity of SYNT. Antagonists may include proteins such as antibodies, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of SYNT either by directly interacting with SYNT or by acting on components of the biological pathway in which SYNT participates.

The term "antibody" refers to intact immunoglobulin molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding an epitopic determinant. Antibodies that bind SYNT polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

The term "antigenic determinant" refers to that region of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (particular regions or three-dimensional structures on the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

The term "antisense" refers to any composition capable of base-pairing with the "sense"

(coding) strand of a specific nucleic acid sequence. Antisense compositions may include DNA; RNA; peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine. Antisense molecules may be produced by any method including chemical synthesis or transcription. Once introduced into a cell, the complementary antisense molecule base-pairs with a naturally occurring nucleic acid sequence produced by the cell to form duplexes which block either transcription or translation. The designation "negative" or "minus" can refer to the antisense strand, and the designation "positive" or "plus" can refer to the sense strand of a reference DNA molecule.

The term "biologically active" refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" or "immunogenic" refers to the capability of the natural, recombinant, or synthetic SYNT, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

"Complementary" describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing. For example, 5'-AGT-3' pairs with its complement, 3'-TCA-5'.

A "composition comprising a given polynucleotide sequence" and a "composition comprising a given amino acid sequence" refer broadly to any composition containing the given polynucleotide or amino acid sequence. The composition may comprise a dry formulation or an aqueous solution. Compositions comprising polynucleotide sequences encoding SYNT or fragments of SYNT may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilizing agent such as a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts (e.g., NaCl), detergents (e.g., sodium dodecyl sulfate; SDS), and other components (e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

"Consensus sequence" refers to a nucleic acid sequence which has been subjected to repeated DNA sequence analysis to resolve uncalled bases, extended using the XL-PCR kit (PE Biosystems, Foster City CA) in the 5' and/or the 3' direction, and resequenced, or which has been assembled from one or more overlapping cDNA, EST, or genomic DNA fragments using a computer program for fragment assembly, such as the GELVIEW fragment assembly system (GCG, Madison WI) or Phrap (University of Washington, Seattle WA). Some sequences have been both extended and assembled to produce the consensus sequence.

"Conservative amino acid substitutions" are those substitutions that are predicted to least interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is conserved and not significantly changed by such substitutions. The table below shows

amino acids which may be substituted for an original amino acid in a protein and which are regarded as conservative amino acid substitutions.

	Original Residue	Conservative Substitution
5	Ala	Gly, Ser
	Arg	His, Lys
	Asn	Asp, Gln, His
	Asp	Asn, Glu
	Cys	Ala, Ser
	Gln	Asn, Glu, His
10	Glu	Asp, Gln, His
	Gly	Ala
	His	Asn, Arg, Gln, Glu
	Ile	Leu, Val
	Leu	Ile, Val
15	Lys	Arg, Gln, Glu
	Met	Leu, Ile
	Phe	His, Met, Leu, Trp, Tyr
	Ser	Cys, Thr
	Thr	Ser, Val
20	Trp	Phe, Tyr
	Tyr	His, Phe, Trp
	Val	Ile, Leu, Thr

Conservative amino acid substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the site of the substitution, and/or (c) the bulk of the side chain.

A "deletion" refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

The term "derivative" refers to a chemically modified polynucleotide or polypeptide. Chemical modifications of a polynucleotide sequence can include, for example, replacement of hydrogen by an alkyl, acyl, hydroxyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one biological or immunological function of the natural molecule. A derivative polypeptide is one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

A "detectable label" refers to a reporter molecule or enzyme that is capable of generating a measurable signal and is covalently or noncovalently joined to a polynucleotide or polypeptide.

A "fragment" is a unique portion of SYNT or the polynucleotide encoding SYNT which is identical in sequence to but shorter in length than the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from 5 to 1000 contiguous nucleotides or amino acid residues. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10,

15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous nucleotides or amino acid residues in length. Fragments may be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50% of a polypeptide) as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the Sequence Listing, tables, and figures, may be encompassed by the present embodiments.

A fragment of SEQ ID NO:16-30 comprises a region of unique polynucleotide sequence that specifically identifies SEQ ID NO:16-30, for example, as distinct from any other sequence in the genome from which the fragment was obtained. A fragment of SEQ ID NO:16-30 is useful, for example, in hybridization and amplification technologies and in analogous methods that distinguish SEQ ID NO:16-30 from related polynucleotide sequences. The precise length of a fragment of SEQ ID NO:16-30 and the region of SEQ ID NO:16-30 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A fragment of SEQ ID NO:1-15 is encoded by a fragment of SEQ ID NO:16-30. A fragment of SEQ ID NO:1-15 comprises a region of unique amino acid sequence that specifically identifies SEQ ID NO:1-15. For example, a fragment of SEQ ID NO:1-15 is useful as an immunogenic peptide for the development of antibodies that specifically recognize SEQ ID NO:1-15. The precise length of a fragment of SEQ ID NO:1-15 and the region of SEQ ID NO:1-15 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A "full-length" polynucleotide sequence is one containing at least a translation initiation codon (e.g., methionine) followed by an open reading frame and a translation termination codon. A "full-length" polynucleotide sequence encodes a "full-length" polypeptide sequence.

"Homology" refers to sequence similarity or, interchangeably, sequence identity, between two or more polynucleotide sequences or two or more polypeptide sequences.

The terms "percent identity" and "% identity," as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences.

Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and P.M. Sharp (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS

8:189-191. For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5, window=4, and "diagonals saved"=4. The "weighted" residue weight table is selected as the default. Percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polynucleotide sequences.

- 5 Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at <http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence
- 10 analysis programs including "blastn," that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at <http://www.ncbi.nlm.nih.gov/gorf/bl2.html>. The "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST
- 15 programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.12 (April-21-2000) set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Reward for match: 1

20 *Penalty for mismatch: -2*

Open Gap: 5 and Extension Gap: 2 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 11

25 *Filter: on*

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous

30 nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures, or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

- Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes
- 35 in a nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

The phrases "percent identity" and "% identity," as applied to polypeptide sequences, refer to the percentage of residue matches between at least two polypeptide sequences aligned using a standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the charge and hydrophobicity at the site of substitution, thus preserving the structure (and therefore function) of the polypeptide.

Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and "diagonals saved"=5. The PAM250 matrix is selected as the default residue weight table. As with polynucleotide alignments, the percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polypeptide sequence pairs.

Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the "BLAST 2 Sequences" tool Version 2.0.12 (Apr-21-2000) with blastp set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Open Gap: 11 and Extension Gap: 1 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 3

Filter: on

Percent identity may be measured over the length of an entire defined polypeptide sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

"Human artificial chromosomes" (HACs) are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size, and which contain all of the elements required for chromosome replication, segregation and maintenance.

The term "humanized antibody" refers to an antibody molecule in which the amino acid sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

“Hybridization” refers to the process by which a polynucleotide strand anneals with a complementary strand through base pairing under defined hybridization conditions. Specific hybridization is an indication that two nucleic acid sequences share a high degree of complementarity. Specific hybridization complexes form under permissive annealing conditions and remain hybridized after the “washing” step(s). The washing step(s) is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid strands that are not perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable by one of ordinary skill in the art and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency, and therefore hybridization specificity. Permissive annealing conditions occur, for example, at 68°C in the presence of about 6 x SSC, about 1% (w/v) SDS, and about 100 µg/ml sheared, denatured salmon sperm DNA.

Generally, stringency of hybridization is expressed, in part, with reference to the temperature under which the wash step is carried out. Such wash temperatures are typically selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and conditions for nucleic acid hybridization are well known and can be found in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour. Alternatively, temperatures of about 65°C, 60°C, 55°C, or 42°C may be used. SSC concentration may be varied from about 0.1 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, sheared and denatured salmon sperm DNA at about 100-200 µg/ml. Organic solvent, such as formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as for RNA:DNA hybridizations. Useful variations on these wash conditions will be readily apparent to those of ordinary skill in the art. Hybridization, particularly under high stringency conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their encoded polypeptides.

The term “hybridization complex” refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., C_0t or R_0t analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate

to which cells or their nucleic acids have been fixed).

The words "insertion" and "addition" refer to changes in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively.

"Immune response" can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

An "immunogenic fragment" is a polypeptide or oligopeptide fragment of SYNT which is capable of eliciting an immune response when introduced into a living organism, for example, a mammal. The term "immunogenic fragment" also includes any polypeptide or oligopeptide fragment of SYNT which is useful in any of the antibody production methods disclosed herein or known in the art.

The term "microarray" refers to an arrangement of a plurality of polynucleotides, polypeptides, or other chemical compounds on a substrate.

The terms "element" and "array element" refer to a polynucleotide, polypeptide, or other chemical compound having a unique and defined position on a microarray.

The term "modulate" refers to a change in the activity of SYNT. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of SYNT.

The phrases "nucleic acid" and "nucleic acid sequence" refer to a nucleotide, oligonucleotide, polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material.

"Operably linked" refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with a second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

"Peptide nucleic acid" (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell.

"Post-translational modification" of an SYNT may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the art. These processes may occur synthetically or biochemically. Biochemical modifications will

vary by cell type depending on the enzymatic milieu of SYNT.

"Probe" refers to nucleic acid sequences encoding SYNT, their complements, or fragments thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule.

5 Typical labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes.

"Primers" are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

10 Probes and primers as used in the present invention typically comprise at least 15 contiguous nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the
15 specification, including the tables, figures, and Sequence Listing, may be used.

Methods for preparing and using probes and primers are described in the references, for example Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; Ausubel, F.M. et al., 1987, Current Protocols in Molecular Biology, Greene Publ. Assoc. & Wiley-Intersciences, New York NY; Innis, M. et al., 1990, PCR
20 Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA. PCR primer pairs can be derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

Oligonucleotides for use as primers are selected using software known in the art for such
25 purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of
30 Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the
35 selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user's specific

needs.) The PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both
5 unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

10 A "recombinant nucleic acid" is a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two or more otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook, supra. The term recombinant includes nucleic acids that have
15 been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a
20 vaccinia virus, that could be used to vaccinate a mammal wherein the recombinant nucleic acid is expressed, inducing a protective immunological response in the mammal.

A "regulatory element" refers to a nucleic acid sequence usually derived from untranslated regions of a gene and includes enhancers, promoters, introns, and 5' and 3' untranslated regions (UTRs). Regulatory elements interact with host or viral proteins which control transcription,
25 translation, or RNA stability.

"Reporter molecules" are chemical or biochemical moieties used for labeling a nucleic acid, amino acid, or antibody. Reporter molecules include radionuclides; enzymes; fluorescent, chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and other moieties known in the art.

30 An "RNA equivalent," in reference to a DNA sequence, is composed of the same linear sequence of nucleotides as the reference DNA sequence with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The term "sample" is used in its broadest sense. A sample suspected of containing nucleic
35 acids encoding SYNT, or fragments thereof, or SYNT itself, may comprise a bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or

cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

The terms "specific binding" and "specifically binding" refer to that interaction between a protein or peptide and an agonist, an antibody, an antagonist, a small molecule, or any natural or synthetic binding composition. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide comprising the epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

The term "substantially purified" refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other components with which they are naturally associated.

A "substitution" refers to the replacement of one or more amino acid residues or nucleotides by different amino acid residues or nucleotides, respectively.

"Substrate" refers to any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

A "transcript image" refers to the collective pattern of gene expression by a particular cell type or tissue under given conditions at a given time.

"Transformation" describes a process by which exogenous DNA is introduced into a recipient cell. Transformation may occur under natural or artificial conditions according to various methods well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based on the type of host cell being transformed and may include, but is not limited to, bacteriophage or viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term "transformed" cells includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for limited periods of time.

A "transgenic organism," as used herein, is any organism, including but not limited to animals and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or in vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The

transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, plants, and animals. The isolated DNA of the present invention can be introduced into the host by methods known in the art, for example infection, transfection, transformation or transconjugation. Techniques for transferring the DNA of the present invention into such organisms are widely known and provided in references such as Sambrook et al. (1989), supra.

A "variant" of a particular nucleic acid sequence is defined as a nucleic acid sequence having at least 40% sequence identity to the particular nucleic acid sequence over a certain length of one of the nucleic acid sequences using blastn with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of nucleic acids may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95% or at least 98% or greater sequence identity over a certain defined length. A variant may be described as, for example, an "allelic" (as defined above), "splice," "species," or "polymorphic" variant. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternative splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one nucleotide base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at least 40% sequence identity to the particular polypeptide sequence over a certain length of one of the polypeptide sequences using blastp with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or at least 98% or greater sequence identity over a certain defined length of one of the polypeptides.

30 THE INVENTION

The invention is based on the discovery of new human synthetases (SYNT), the polynucleotides encoding SYNT, and the use of these compositions for the diagnosis, treatment, or prevention of immune, neuronal, and reproductive disorders, and cell proliferative disorders including cancer.

35 Table 1 lists the Incyte clones used to assemble full length nucleotide sequences encoding SYNT. Columns 1 and 2 show the sequence identification numbers (SEQ ID NOs) of the polypeptide

and nucleotide sequences, respectively. Column 3 shows the clone IDs of the Incyte clones in which nucleic acids encoding each SYNT were identified, and column 4 shows the cDNA libraries from which these clones were isolated. Column 5 shows Incyte clones and their corresponding cDNA libraries. Clones for which cDNA libraries are not indicated were derived from pooled cDNA libraries. In some cases, GenBank sequence identifiers are also shown in column 5. The Incyte clones and GenBank cDNA sequences, where indicated, in column 5 were used to assemble the consensus nucleotide sequence of each SYNT and are useful as fragments in hybridization technologies.

The columns of Table 2 show various properties of each of the polypeptides of the invention: column 1 references the SEQ ID NO; column 2 shows the number of amino acid residues in each polypeptide; column 3 shows potential phosphorylation sites; column 4 shows potential glycosylation sites; column 5 shows the amino acid residues comprising signature sequences and motifs; column 6 shows homologous sequences as identified by BLAST analysis; and column 7 shows analytical methods and in some cases, searchable databases to which the analytical methods were applied. The methods of column 7 were used to characterize each polypeptide through sequence homology and protein motifs.

The columns of Table 3 show the tissue-specificity and diseases, disorders, or conditions associated with nucleotide sequences encoding SYNT. The first column of Table 3 lists the nucleotide SEQ ID NOs. Column 2 lists fragments of the nucleotide sequences of column 1. These fragments are useful, for example, in hybridization or amplification technologies to identify SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19 SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:29, and SEQ ID NO:30 and to distinguish between SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19 SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:29, and SEQ ID NO:30 and related polynucleotide sequences. The polypeptides encoded by these fragments are useful, for example, as immunogenic peptides. Column 3 lists tissue categories which express SYNT as a fraction of total tissues expressing SYNT. Column 4 lists diseases, disorders, or conditions associated with those tissues expressing SYNT as a fraction of total tissues expressing SYNT. Column 5 lists the vectors used to subclone each cDNA library.

The columns of Table 4 show descriptions of the tissues used to construct the cDNA libraries from which cDNA clones encoding SYNT were isolated. Column 1 references the nucleotide SEQ ID NOs, column 2 shows the cDNA libraries from which these clones were isolated, and column 3 shows the tissue origins and other descriptive information relevant to the cDNA libraries in column 2.

SEQ ID NO: 16 maps to chromosome 5 within the interval from 147.10 to 150.00 centiMorgans. SEQ ID NO: 17 maps to chromosome 10 within the interval from 137.60 to 139.20 centiMorgans. This interval also contains gene MXI1, a member of the MYC family. SEQ ID NO:

18 maps to chromosome 2 within the interval from 228.80 to 230.10 centiMorgans. This interval also contains a gene for a proto-oncogene encoding a tyrosine-protein kinase. SEQ ID NO:21 maps to chromosome 5 within the interval from 172.6 to 184.7 centiMorgans. SEQ ID NO:24 maps to chromosome 2 within the interval from 118.0 to 127.4 centiMorgans. SEQ ID NO:26 maps to chromosome 3 within the interval from 157.4 to 162.0 centiMorgans. SEQ ID NO:27 maps to chromosome 12 within the interval from 97.1 to 116.6 centiMorgans. SEQ ID NO:28 maps to chromosome 4 within the interval from 77.3 to 99.2 centiMorgans and to chromosome 5 within the intervals from 79.2 to 92.3 centiMorgans, from 116.3 to 127.9 centiMorgans, and from 157.6 to 163.0 centiMorgans. SEQ ID NO:29 maps to chromosome 1 within the interval from 242.5 to 258.7 centiMorgans and to chromosome 19 within the interval from 69.9 to 104.9 centiMorgans. SEQ ID NO:30 maps to chromosome 1 within the interval from 57.2 to 57.5 centiMorgans.

The invention also encompasses SYNT variants. A preferred SYNT variant is one which has at least about 80%, or alternatively at least about 90%, or even at least about 95% amino acid sequence identity to the SYNT amino acid sequence, and which contains at least one functional or structural characteristic of SYNT.

The invention also encompasses polynucleotides which encode SYNT. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:16-30, which encodes SYNT. The polynucleotide sequences of SEQ ID NO:16-30, as presented in the Sequence Listing, embrace the equivalent RNA sequences, wherein occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The invention also encompasses a variant of a polynucleotide sequence encoding SYNT. In particular, such a variant polynucleotide sequence will have at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to the polynucleotide sequence encoding SYNT. A particular aspect of the invention encompasses a variant of a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:16-30 which has at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:16-30. Any one of the polynucleotide variants described above can encode an amino acid sequence which contains at least one functional or structural characteristic of SYNT.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding SYNT, some bearing minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible variation of polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the

polynucleotide sequence of naturally occurring SYNT, and all such variations are to be considered as being specifically disclosed.

Although nucleotide sequences which encode SYNT and its variants are generally capable of hybridizing to the nucleotide sequence of the naturally occurring SYNT under appropriately selected
5 conditions of stringency, it may be advantageous to produce nucleotide sequences encoding SYNT or its derivatives possessing a substantially different codon usage, e.g., inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide
10 sequence encoding SYNT and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

The invention also encompasses production of DNA sequences which encode SYNT and SYNT derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the
15 synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding SYNT or any fragment thereof.

Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID
20 NO:16-30 and fragments thereof under various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511.) Hybridization conditions, including annealing and wash conditions, are described in "Definitions."

Methods for DNA sequencing are well known in the art and may be used to practice any of
25 the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (PE Biosystems, Foster City CA), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies, Gaithersburg MD). Preferably,
30 sequence preparation is automated with machines such as the MICROLAB 2200 liquid transfer system (Hamilton, Reno NV), PTC200 thermal cycler (MJ Research, Watertown MA) and ABI CATALYST 800 thermal cycler (PE Biosystems). Sequencing is then carried out using either the ABI 373 or 377 DNA sequencing system (PE Biosystems), the MEGABACE 1000 DNA sequencing system (Molecular Dynamics, Sunnyvale CA), or other systems known in the art. The resulting
35 sequences are analyzed using a variety of algorithms which are well known in the art. (See, e.g., Ausubel, F.M. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY, unit

7.7: Meyers, R.A. (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853.)

The nucleic acid sequences encoding SYNT may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) PCR Methods Applic. 2:318-322.) Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences. (See, e.g., Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and yeast artificial chromosome DNA. (See, e.g., Lagerstrom, M. et al. (1991) PCR Methods Applic. 1:111-119.) In this method, multiple restriction enzyme digestions and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR. Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) Nucleic Acids Res. 19:3055-3060). Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 Primer Analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to 72°C.

When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5' non-transcribed regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, PE Biosystems), and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments

which may be present in limited amounts in a particular sample.

In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode SYNT may be cloned in recombinant DNA molecules that direct expression of SYNT, or fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent
5 degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be produced and used to express SYNT.

The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter SYNT-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA
10 shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

The nucleotides of the present invention may be subjected to DNA shuffling techniques such
15 as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent Number 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat. Biotechnol. 17:259-264; and Crameri, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve the biological properties of SYNT, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene
20 variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random
25 point mutations may be recombined, screened, and then reshuffled until the desired properties are optimized. Alternatively, fragments of a given gene may be recombined with fragments of homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

In another embodiment, sequences encoding SYNT may be synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) Nucleic Acids Symp. Ser. 7:215-223; and Horn, T. et al. (1980) Nucleic Acids Symp. Ser. 7:225-232.)
Alternatively, SYNT itself or a fragment thereof may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solution-phase or solid-phase techniques.
35 (See, e.g., Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH Freeman, New York NY, pp. 55-60; and Roberge, J.Y. et al. (1995) Science 269:202-204.) Automated synthesis

may be achieved using the ABI 431A peptide synthesizer (PE Biosystems). Additionally, the amino acid sequence of SYNT, or any part thereof, may be altered during direct synthesis and/or combined with sequences from other proteins, or any part thereof, to produce a variant polypeptide or a polypeptide having a sequence of a naturally occurring polypeptide.

5 The peptide may be substantially purified by preparative high performance liquid chromatography. (See, e.g., Chiez, R.M. and F.Z. Regnier (1990) *Methods Enzymol.* 182:392-421.) The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing. (See, e.g., Creighton, *supra*, pp. 28-53.)

10 In order to express a biologically active SYNT, the nucleotide sequences encoding SYNT or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements include regulatory sequences, such as enhancers, constitutive and inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotide sequences encoding SYNT. Such elements may vary in their strength and specificity. Specific initiation signals
15 may also be used to achieve more efficient translation of sequences encoding SYNT. Such signals include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where sequences encoding SYNT and its initiation codon and upstream regulatory sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted,
20 exogenous translational control signals including an in-frame ATG initiation codon should be provided by the vector. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the particular host cell system used. (See, e.g., Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162.)

25 Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding SYNT and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. (See, e.g., Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY, ch. 4, 8, and 16-17; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, ch. 9, 13, and
30 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences encoding SYNT. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with
35 yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV,

or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems. (See, e.g., Sambrook, supra; Ausubel, supra; Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509; Bitter, G.A. et al. (1987) Methods Enzymol. 153:516-544; Scorer, C.A. et al. (1994) Bio/Technology 12:181-184; Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945; Takamatsu, N. (1987) EMBO J. 6:307-311; Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie, R. et al. (1984) Science 224:838-843; Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196; Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659; and Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.) Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. (See, e.g., Di Nicola, M. et al. (1998) Cancer Gen. Ther. 5(6):350-356; Yu, M. et al., (1993) Proc. Natl. Acad. Sci. USA 90(13):6340-6344; Buller, R.M. et al. (1985) Nature 317(6040):813-815; McGregor, D.P. et al. (1994) Mol. Immunol. 31(3):219-226; and Verma, I.M. and N. Somia (1997) Nature 389:239-242.) The invention is not limited by the host cell employed.

In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding SYNT. For example, routine cloning, subcloning, and propagation of polynucleotide sequences encoding SYNT can be achieved using a multifunctional *E. coli* vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or PSPORT1 plasmid (Life Technologies). Ligation of sequences encoding SYNT into the vector's multiple cloning site disrupts the *lacZ* gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for *in vitro* transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509.) When large quantities of SYNT are needed, e.g. for the production of antibodies, vectors which direct high level expression of SYNT may be used. For example, vectors containing the strong, inducible T5 or T7 bacteriophage promoter may be used.

Yeast expression systems may be used for production of SYNT. A number of vectors containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH promoters, may be used in the yeast *Saccharomyces cerevisiae* or *Pichia pastoris*. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel, 1995, supra; Bitter, supra; and Scorer, supra.)

Plant systems may also be used for expression of SYNT. Transcription of sequences encoding SYNT may be driven viral promoters, e.g., the 35S and 19S promoters of CaMV used alone

or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) EMBO J. 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used. (See, e.g., Coruzzi, supra; Broglie, supra; and Winter, supra.) These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. (See, e.g., The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196.)

In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding SYNT may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain infective virus which expresses SYNT in host cells. (See, e.g., Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.)

For long term production of recombinant proteins in mammalian systems, stable expression of SYNT in cell lines is preferred. For example, sequences encoding SYNT can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to confer resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine phosphoribosyltransferase genes, for use in *tk*⁻ and *apr*⁻ cells, respectively. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* and *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g., Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981)

J. Mol. Biol. 150:1-14.) Additional selectable genes have been described, e.g., *trpB* and *hisD*, which alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), β glucuronidase and its substrate β -glucuronide, or luciferase and its substrate luciferin may be used. These markers can be used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system. (See, e.g., Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, the presence and expression of the gene may need to be confirmed. For example, if the sequence encoding SYNT is inserted within a marker gene sequence, transformed cells containing sequences encoding SYNT can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding SYNT under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

In general, host cells that contain the nucleic acid sequence encoding SYNT and that express SYNT may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein sequences.

Immunological methods for detecting and measuring the expression of SYNT using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on SYNT is preferred, but a competitive binding assay may be employed. These and other assays are well known in the art. (See, e.g., Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press, St. Paul MN, Sect. IV; Coligan, J.E. et al. (1997) Current Protocols in Immunology, Greene Pub. Associates and Wiley-Interscience, New York NY; and Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa NJ.)

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding SYNT include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding SYNT, or any fragments thereof, may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase

such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits, such as those provided by Amersham Pharmacia Biotech, Promega (Madison WI), and US Biochemical. Suitable reporter molecules or labels which may be used for ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with nucleotide sequences encoding SYNT may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode SYNT may be designed to contain signal sequences which direct secretion of SYNT through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" or "pro" form of the protein may also be used to specify protein targeting, folding, and/or activity. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38) are available from the American Type Culture Collection (ATCC, Manassas VA) and may be chosen to ensure the correct modification and processing of the foreign protein.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding SYNT may be ligated to a heterologous sequence resulting in translation of a fusion protein in any of the aforementioned host systems. For example, a chimeric SYNT protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of SYNT activity. Heterologous protein and peptide moieties may also facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metal-chelate resins, respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the SYNT encoding sequence and the heterologous protein sequence, so that SYNT may be cleaved away from the heterologous moiety following purification. Methods for fusion protein expression and purification are discussed in Ausubel (1995, supra, ch. 10).

A variety of commercially available kits may also be used to facilitate expression and purification of fusion proteins.

In a further embodiment of the invention, synthesis of radiolabeled SYNT may be achieved in vitro using the TNT rabbit reticulocyte lysate or wheat germ extract system (Promega). These

5 systems couple transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, for example, ³⁵S-methionine.

SYNT of the present invention or fragments thereof may be used to screen for compounds that specifically bind to SYNT. At least one and up to a plurality of test compounds may be screened
10 for specific binding to SYNT. Examples of test compounds include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

In one embodiment, the compound thus identified is closely related to the natural ligand of SYNT, e.g., a ligand or fragment thereof, a natural substrate, a structural or functional mimetic, or a natural binding partner. (See, Coligan, J.E. et al. (1991) Current Protocols in Immunology 1(2):
15 Chapter 5.) Similarly, the compound can be closely related to the natural receptor to which SYNT binds, or to at least a fragment of the receptor, e.g., the ligand binding site. In either case, the compound can be rationally designed using known techniques. In one embodiment, screening for these compounds involves producing appropriate cells which express SYNT, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or
20 E. coli. Cells expressing SYNT or cell membrane fractions which contain SYNT are then contacted with a test compound and binding, stimulation, or inhibition of activity of either SYNT or the compound is analyzed.

An assay may simply test binding of a test compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. For example,
25 the assay may comprise the steps of combining at least one test compound with SYNT, either in solution or affixed to a solid support, and detecting the binding of SYNT to the compound. Alternatively, the assay may detect or measure binding of a test compound in the presence of a labeled competitor. Additionally, the assay may be carried out using cell-free preparations, chemical libraries, or natural product mixtures, and the test compound(s) may be free in solution or affixed to a
30 solid support.

SYNT of the present invention or fragments thereof may be used to screen for compounds that modulate the activity of SYNT. Such compounds may include agonists, antagonists, or partial or inverse agonists. In one embodiment, an assay is performed under conditions permissive for SYNT activity, wherein SYNT is combined with at least one test compound, and the activity of SYNT in the
35 presence of a test compound is compared with the activity of SYNT in the absence of the test compound. A change in the activity of SYNT in the presence of the test compound is indicative of a

compound that modulates the activity of SYNT. Alternatively, a test compound is combined with an in vitro or cell-free system comprising SYNT under conditions suitable for SYNT activity, and the assay is performed. In either of these assays, a test compound which modulates the activity of SYNT may do so indirectly and need not come in direct contact with the test compound. At least one and up to a plurality of test compounds may be screened.

In another embodiment, polynucleotides encoding SYNT or their mammalian homologs may be "knocked out" in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of human disease. (See, e.g., U.S. Patent No. 5,175,383 and U.S. Patent No. 5,767,337.) For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the gene of interest disrupted by a marker gene, e.g., the neomycin phosphotransferase gene (neo; Capecchi, M.R. (1989) Science 244:1288-1292). The vector integrates into the corresponding region of the host genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D. (1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic Acids Res. 25:4323-4330). Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential therapeutic or toxic agents.

Polynucleotides encoding SYNT may also be manipulated in vitro in ES cells derived from human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

Polynucleotides encoding SYNT can also be used to create "knockin" humanized animals (pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of a polynucleotide encoding SYNT is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and treated with potential pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to overexpress SYNT, e.g., by secreting SYNT in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) Biotechnol. Annu. Rev. 4:55-74).

THERAPEUTICS

Chemical and structural similarity, e.g., in the context of sequences and motifs, exists

- between regions of SYNT and human synthetases. In addition, the expression of SYNT is closely associated with hematopoietic/immune, cancerous, proliferating, inflamed, immune, nervous, gastrointestinal and reproductive tissues. Therefore, SYNT appears to play a role in an immune disorder such as inflammation, actinic keratosis, acquired immunodeficiency syndrome (AIDS),
- 5 Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, arteriosclerosis, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, bronchitis, bursitis, cholecystitis, cirrhosis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease,
 - 10 Hashimoto's thyroiditis, paroxysmal nocturnal hemoglobinuria, hepatitis, hypereosinophilia, irritable bowel syndrome, episodic lymphopenia with lymphocytotoxins, mixed connective tissue disease (MCTD), multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, myelofibrosis, osteoarthritis, osteoporosis, pancreatitis, polycythemia vera, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis,
 - 15 systemic lupus erythematosus, systemic sclerosis, primary thrombocythemia, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, trauma, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and hematopoietic cancer including lymphoma, leukemia, and myeloma; a neuronal disorder, such as akathisia, Alzheimer's disease, amnesia, amyotrophic lateral sclerosis, bipolar
 - 20 disorder, catatonia, cerebral neoplasms, dementia, depression, diabetic neuropathy, Down's syndrome, tardive dyskinesia, dystonias, epilepsy, Huntington's disease, peripheral neuropathy, multiple sclerosis, neurofibromatosis, Parkinson's disease, paranoid psychoses, postherpetic neuralgia, schizophrenia, and Tourette's disorder; a reproductive disorder, such as a disorder of prolactin production, infertility, including tubal disease, ovulatory defects, and endometriosis, a disruption of
 - 25 the estrous cycle, a disruption of the menstrual cycle, polycystic ovary syndrome, ovarian hyperstimulation syndrome, an endometrial or ovarian tumor, a uterine fibroid, autoimmune disorders, an ectopic pregnancy, and teratogenesis; cancer of the breast, fibrocystic breast disease, and galactorrhea; a disruption of spermatogenesis, abnormal sperm physiology, cancer of the testis, cancer of the prostate, benign prostatic hyperplasia, prostatitis, Peyronie's disease, impotence,
 - 30 carcinoma of the male breast, and gynecomastia; and a cell proliferative disorder, such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, a cancer of the adrenal gland, bladder, bone,
 - 35 bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis,

thymus, thyroid, and uterus.

In another embodiment, a vector capable of expressing SYNT or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of SYNT including, but not limited to, those described above.

5 In a further embodiment, a pharmaceutical composition comprising a substantially purified SYNT in conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of SYNT including, but not limited to, those provided above.

10 In still another embodiment, an agonist which modulates the activity of SYNT may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of SYNT including, but not limited to, those listed above.

In a further embodiment, an antagonist of SYNT may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of SYNT. Examples of such disorders include, but are not limited to, those immune, neuronal, reproductive, and cell proliferative
15 disorders described above. In one aspect, an antibody which specifically binds SYNT may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissues which express SYNT.

In an additional embodiment, a vector expressing the complement of the polynucleotide encoding SYNT may be administered to a subject to treat or prevent a disorder associated with
20 increased expression or activity of SYNT including, but not limited to, those described above.

In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The
25 combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

An antagonist of SYNT may be produced using methods which are generally known in the art. In particular, purified SYNT may be used to produce antibodies or to screen libraries of
30 pharmaceutical agents to identify those which specifically bind SYNT. Antibodies to SYNT may also be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies (i.e., those which inhibit dimer formation) are generally preferred for therapeutic use.

35 For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and others may be immunized by injection with SYNT or with any fragment or oligopeptide thereof

which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to SYNT have an amino acid sequence consisting of at least about 5 amino acids, and generally will consist of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are identical to a portion of the amino acid sequence of the natural protein. Short stretches of SYNT amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

Monoclonal antibodies to SYNT may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique. (See, e.g., Kohler, G. et al. (1975) Nature 256:495-497; Kozbor, D. et al. (1985) J. Immunol. Methods 81:31-42; Cote, R.J. et al. (1983) Proc. Natl. Acad. Sci. USA 80:2026-2030; and Cole, S.P. et al. (1984) Mol. Cell Biol. 62:109-120.)

In addition, techniques developed for the production of "chimeric antibodies," such as the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984) Proc. Natl. Acad. Sci. USA 81:6851-6855; Neuberger, M.S. et al. (1984) Nature 312:604-608; and Takeda, S. et al. (1985) Nature 314:452-454.) Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce SYNT-specific single chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g., Burton, D.R. (1991) Proc. Natl. Acad. Sci. USA 88:10134-10137.)

Antibodies may also be produced by inducing in vivo production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature. (See, e.g., Orlandi, R. et al. (1989) Proc. Natl. Acad. Sci. USA 86:3833-3837; Winter, G. et al. (1991) Nature 349:293-299.)

Antibody fragments which contain specific binding sites for SYNT may also be generated. For example, such fragments include, but are not limited to, F(ab')₂ fragments produced by pepsin digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D. et al. (1989) Science 246:1275-1281.)

Various immunoassays may be used for screening to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between SYNT and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering SYNT epitopes is generally used, but a competitive binding assay may also be employed (Pound, supra).

Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for SYNT. Affinity is expressed as an association constant, K_a , which is defined as the molar concentration of SYNT-antibody complex divided by the molar concentrations of free antigen and free antibody under equilibrium conditions. The K_a determined for a preparation of polyclonal antibodies, which are heterogeneous in their affinities for multiple SYNT epitopes, represents the average affinity, or avidity, of the antibodies for SYNT. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular SYNT epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a ranging from about 10^9 to 10^{12} L/mole are preferred for use in immunoassays in which the SYNT-antibody complex must withstand rigorous manipulations. Low-affinity antibody preparations with K_a ranging from about 10^6 to 10^7 L/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of SYNT, preferably in active form, from the antibody (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington DC; Liddell, J.E. and A. Cryer (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to determine the quality and suitability of such preparations for certain downstream applications. For example, a polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is generally employed in procedures requiring precipitation of SYNT-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines for antibody quality and usage in various applications, are generally available. (See, e.g., Catty, supra, and Coligan et al., supra.)

In another embodiment of the invention, the polynucleotides encoding SYNT, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, modifications of gene expression can be achieved by designing complementary sequences or antisense molecules (DNA, RNA, PNA, or modified oligonucleotides) to the coding or regulatory regions of the gene encoding SYNT. Such technology is well known in the art, and antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding SYNT. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc.,

Totawa NJ.)

In therapeutic use, any gene delivery system suitable for introduction of the antisense sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence complementary to at least a portion of the cellular sequence encoding the target protein. (See, e.g., Slater, J.E. et al. (1998) *J. Allergy Clin. Immunol.* 102(3):469-475; and Scanlon, K.J. et al. (1995) 9(13):1288-1296.) Antisense sequences can also be introduced intracellularly through the use of viral vectors, such as retrovirus and adeno-associated virus vectors. (See, e.g., Miller, A.D. (1990) *Blood* 76:271; Ausubel, *supra*; Uckert, W. and W. Walther (1994) *Pharmacol. Ther.* 63(3):323-347.) Other gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art. (See, e.g., Rossi, J.J. (1995) *Br. Med. Bull.* 51(1):217-225; Boado, R.J. et al. (1998) *J. Pharm. Sci.* 87(11):1308-1315; and Morris, M.C. et al. (1997) *Nucleic Acids Res.* 25(14):2730-2736.)

In another embodiment of the invention, polynucleotides encoding SYNT may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) *Science* 288:669-672), severe combined immunodeficiency syndrome associated with an inherited adenosine deaminase (ADA) deficiency (Blaese, R.M. et al. (1995) *Science* 270:475-480; Bordignon, C. et al. (1995) *Science* 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) *Cell* 75:207-216; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:643-666; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:667-703), thalassemias, familial hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal, R.G. (1995) *Science* 270:404-410; Verma, I.M. and Somia, N. (1997) *Nature* 389:239-242)), (ii) express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) *Nature* 335:395-396; Poeschla, E. et al. (1996) *Proc. Natl. Acad. Sci. USA.* 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites, such as Candida albicans and Paracoccidioides brasiliensis; and protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in SYNT expression or regulation causes disease, the expression of SYNT from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

In a further embodiment of the invention, diseases or disorders caused by deficiencies in SYNT are treated by constructing mammalian expression vectors encoding SYNT and introducing these vectors by mechanical means into SYNT-deficient cells. Mechanical transfer technologies for use with cells *in vivo* or *ex vitro* include (i) direct DNA microinjection into individual cells, (ii)

ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and W.F. Anderson (1993) *Annu. Rev. Biochem.* 62:191-217; Ivics, Z. (1997) *Cell* 91:501-510; Boulay, J.-L. and H. R  cipon (1998) *Curr. Opin. Biotechnol.* 9:445-450).

- 5 Expression vectors that may be effective for the expression of SYNT include, but are not limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX vectors (Invitrogen, Carlsbad CA), PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF, PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). SYNT may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus
- 10 (RSV), SV40 virus, thymidine kinase (TK), or β -actin genes), (ii) an inducible promoter (e.g., the tetracycline-regulated promoter (Gossen, M. and H. Bujard (1992) *Proc. Natl. Acad. Sci. USA* 89:5547-5551; Gossen, M. et al. (1995) *Science* 268:1766-1769; Rossi, F.M.V. and H.M. Blau (1998) *Curr. Opin. Biotechnol.* 9:451-456), commercially available in the T-REX plasmid (Invitrogen)); the ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the
- 15 FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and H.M. Blau, *supra*), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding SYNT from a normal individual.

- Commercially available liposome transformation kits (e.g., the PERFECT LIPID TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver
- 20 polynucleotides to target cells in culture and require minimal effort to optimize experimental parameters. In the alternative, transformation is performed using the calcium phosphate method (Graham, F.L. and A.J. Eb (1973) *Virology* 52:456-467), or by electroporation (Neumann, E. et al. (1982) *EMBO J.* 1:841-845). The introduction of DNA to primary cells requires modification of these standardized mammalian transfection protocols.

- 25 In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to SYNT expression are treated by constructing a retrovirus vector consisting of (i) the polynucleotide encoding SYNT under the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences
- 30 required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) *Proc. Natl. Acad. Sci. USA* 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al.
- 35 (1987) *J. Virol.* 61:1647-1650; Bender, M.A. et al. (1987) *J. Virol.* 61:1639-1646; Adam, M.A. and A.D. Miller (1988) *J. Virol.* 62:3802-3806; Dull, T. et al. (1998) *J. Virol.* 72:8463-8471; Zufferey, R.

et al. (1998) J. Virol. 72:9873-9880). U.S. Patent Number 5,910,434 to Rigg ("Method for obtaining retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant") discloses a method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference. Propagation of retrovirus vectors, transduction of a population of cells (e.g., CD4⁺ T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) J. Virol. 71:7020-7029; Bauer, G. et al. (1997) Blood 89:2259-2267; Bonyhadi, M.L. (1997) J. Virol. 71:4707-4716; Ranga, U. et al. (1998) Proc. Natl. Acad. Sci. USA 95:1201-1206; Su, L. (1997) Blood 89:2283-2290).

In the alternative, an adenovirus-based gene therapy delivery system is used to deliver polynucleotides encoding SYNT to cells which have one or more genetic abnormalities with respect to the expression of SYNT. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) Transplantation 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent Number 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999) Annu. Rev. Nutr. 19:511-544; and Verma, I.M. and N. Somia (1997) Nature 18:389:239-242, both incorporated by reference herein.

In another alternative, a herpes-based, gene therapy delivery system is used to deliver polynucleotides encoding SYNT to target cells which have one or more genetic abnormalities with respect to the expression of SYNT. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing SYNT to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) Exp. Eye Res. 169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent Number 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby incorporated by reference. U.S. Patent Number 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W.F. et al. (1999) J. Virol. 73:519-532 and Xu, H. et al. (1994) Dev. Biol. 163:152-161, hereby incorporated by reference. The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the large herpesvirus genomes, the growth and propagation

of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary skill in the art.

In another alternative, an alphavirus (positive, single-stranded RNA virus) vector is used to deliver polynucleotides encoding SYNT to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based on the SFV genome (Garoff, H. and K.-J. Li (1998) Curr. Opin. Biotech. 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full-length genomic RNA, resulting in the overproduction of capsid proteins relative to the viral proteins with enzymatic activity (e.g., protease and polymerase). Similarly, inserting the coding sequence for SYNT into the alphavirus genome in place of the capsid-coding region results in the production of a large number of SYNT-coding RNAs and the synthesis of high levels of SYNT in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN) indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) Virology 228:74-83). The wide host range of alphaviruses will allow the introduction of SYNT into a variety of cell types. The specific transduction of a subset of cells in a population may require the sorting of cells prior to transduction. The methods of manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA transfections, and performing alphavirus infections, are well known to those with ordinary skill in the art.

Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, may also be employed to inhibit gene expression. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee, J.E. et al. (1994) in Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing, Mt. Kisco NY, pp. 163-177.) A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. For example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding SYNT.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by

scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides, corresponding to the region of the target gene containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis.

Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding SYNT. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

An additional embodiment of the invention encompasses a method for screening for a compound which is effective in altering expression of a polynucleotide encoding SYNT. Compounds which may be effective in altering expression of a specific polynucleotide may include, but are not limited to, oligonucleotides, antisense oligonucleotides, triple helix-forming oligonucleotides, transcription factors and other polypeptide transcriptional regulators, and non-macromolecular chemical entities which are capable of interacting with specific polynucleotide sequences. Effective compounds may alter polynucleotide expression by acting as either inhibitors or promoters of polynucleotide expression. Thus, in the treatment of disorders associated with increased SYNT expression or activity, a compound which specifically inhibits expression of the polynucleotide encoding SYNT may be therapeutically useful, and in the treatment of disorders associated with decreased SYNT expression or activity, a compound which specifically promotes expression of the polynucleotide encoding SYNT may be therapeutically useful.

At least one, and up to a plurality, of test compounds may be screened for effectiveness in altering expression of a specific polynucleotide. A test compound may be obtained by any method

commonly known in the art, including chemical modification of a compound known to be effective in altering polynucleotide expression; selection from an existing, commercially-available or proprietary library of naturally-occurring or non-natural chemical compounds; rational design of a compound based on chemical and/or structural properties of the target polynucleotide; and selection from a library of chemical compounds created combinatorially or randomly. A sample comprising a polynucleotide encoding SYNT is exposed to at least one test compound thus obtained. The sample may comprise, for example, an intact or permeabilized cell, or an *in vitro* cell-free or reconstituted biochemical system. Alterations in the expression of a polynucleotide encoding SYNT are assayed by any method commonly known in the art. Typically, the expression of a specific nucleotide is detected by hybridization with a probe having a nucleotide sequence complementary to the sequence of the polynucleotide encoding SYNT. The amount of hybridization may be quantified, thus forming the basis for a comparison of the expression of the polynucleotide both with and without exposure to one or more test compounds. Detection of a change in the expression of a polynucleotide exposed to a test compound indicates that the test compound is effective in altering the expression of the polynucleotide. A screen for a compound effective in altering expression of a specific polynucleotide can be carried out, for example, using a *Schizosaccharomyces pombe* gene expression system (Atkins, D. et al. (1999) U.S. Patent No. 5,932,435; Arndt, G.M. et al. (2000) Nucleic Acids Res. 28:E15) or a human cell line such as HeLa cell (Clarke, M.L. et al. (2000) Biochem. Biophys. Res. Commun. 268:8-13). A particular embodiment of the present invention involves screening a combinatorial library of oligonucleotides (such as deoxyribonucleotides, ribonucleotides, peptide nucleic acids, and modified oligonucleotides) for antisense activity against a specific polynucleotide sequence (Bruce, T.W. et al. (1997) U.S. Patent No. 5,686,242; Bruce, T.W. et al. (2000) U.S. Patent No. 6,022,691).

Many methods for introducing vectors into cells or tissues are available and equally suitable for use *in vivo*, *in vitro*, and *ex vivo*. For *ex vivo* therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved using methods which are well known in the art. (See, e.g., Goldman, C.K. et al. (1997) Nat. Biotechnol. 15:462-466.)

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as humans, dogs, cats, cows, horses, rabbits, and monkeys.

An additional embodiment of the invention relates to the administration of a pharmaceutical composition which generally comprises an active ingredient formulated with a pharmaceutically acceptable excipient. Excipients may include, for example, sugars, starches, celluloses, gums, and proteins. Various formulations are commonly known and are thoroughly discussed in the latest

edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA). Such pharmaceutical compositions may consist of SYNT, antibodies to SYNT, and mimetics, agonists, antagonists, or inhibitors of SYNT.

The pharmaceutical compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, pulmonary, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

Pharmaceutical compositions for pulmonary administration may be prepared in liquid or dry powder form. These compositions are generally aerosolized immediately prior to inhalation by the patient. In the case of small molecules (e.g. traditional low molecular weight organic drugs), aerosol delivery of fast-acting formulations is well-known in the art. In the case of macromolecules (e.g. larger peptides and proteins), recent developments in the field of pulmonary delivery via the alveolar region of the lung have enabled the practical delivery of drugs such as insulin to blood circulation (see, e.g., Patton, J.S. et al., U.S. Patent No. 5,997,848). Pulmonary delivery has the advantage of administration without needle injection, and obviates the need for potentially toxic penetration enhancers.

Pharmaceutical compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

Specialized forms of pharmaceutical compositions may be prepared for direct intracellular delivery of macromolecules comprising SYNT or fragments thereof. For example, liposome preparations containing a cell-impermeable macromolecule may promote cell fusion and intracellular delivery of the macromolecule. Alternatively, SYNT or a fragment thereof may be joined to a short cationic N-terminal portion from the HIV Tat-1 protein. Fusion proteins thus generated have been found to transduce into the cells of all tissues, including the brain, in a mouse model system (Schwarze, S.R. et al. (1999) Science 285:1569-1572).

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells, or in animal models such as mice, rats, rabbits, dogs, monkeys, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example SYNT or fragments thereof, antibodies of SYNT, and agonists, antagonists or inhibitors of SYNT, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED₅₀ (the dose therapeutically effective in 50% of the population) or LD₅₀ (the dose

lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic effects is the therapeutic index, which can be expressed as the LD_{50}/ED_{50} ratio. Pharmaceutical compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED_{50} with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. Long-acting pharmaceutical compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about $0.1 \mu\text{g}$ to $100,000 \mu\text{g}$, up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

In another embodiment, antibodies which specifically bind SYNT may be used for the diagnosis of disorders characterized by expression of SYNT, or in assays to monitor patients being treated with SYNT or agonists, antagonists, or inhibitors of SYNT. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for SYNT include methods which utilize the antibody and a label to detect SYNT in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known in the art and may be used.

A variety of protocols for measuring SYNT, including ELISAs, RIAs, and FACS, are known in the art and provide a basis for diagnosing altered or abnormal levels of SYNT expression. Normal or standard values for SYNT expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, for example, human subjects, with antibody to SYNT under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, such as photometric means. Quantities of SYNT expressed in

subject, control, and disease samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding SYNT may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantify gene expression in biopsied tissues in which expression of SYNT may be correlated with disease. The diagnostic assay may be used to determine absence, presence, and excess expression of SYNT, and to monitor regulation of SYNT levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding SYNT or closely related molecules may be used to identify nucleic acid sequences which encode SYNT. The specificity of the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification will determine whether the probe identifies only naturally occurring sequences encoding SYNT, allelic variants, or related sequences.

Probes may also be used for the detection of related sequences, and may have at least 50% sequence identity to any of the SYNT encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be derived from the sequence of SEQ ID NO:16-30 or from genomic sequences including promoters, enhancers, and introns of the SYNT gene.

Means for producing specific hybridization probes for DNAs encoding SYNT include the cloning of polynucleotide sequences encoding SYNT or SYNT derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ^{32}P or ^{35}S , or by enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotide sequences encoding SYNT may be used for the diagnosis of disorders associated with expression of SYNT. Examples of such disorders include, but are not limited to, an immune disorder such as inflammation, actinic keratosis, acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, arteriosclerosis, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, bronchitis, bursitis, cholecystitis, cirrhosis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, paroxysmal nocturnal hemoglobinuria, hepatitis, hypereosinophilia, irritable bowel syndrome, episodic lymphopenia with lymphocytotoxins, mixed connective tissue

disease (MCTD), multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, myelofibrosis, osteoarthritis, osteoporosis, pancreatitis, polycythemia vera, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, primary thrombocythemia, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, trauma, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and hematopoietic cancer including lymphoma, leukemia, and myeloma; a neuronal disorder, such as akathisia, Alzheimer's disease, amnesia, amyotrophic lateral sclerosis, bipolar disorder, catatonia, cerebral neoplasms, dementia, depression, diabetic neuropathy, Down's syndrome, tardive dyskinesia, dystonias, epilepsy, Huntington's disease, peripheral neuropathy, multiple sclerosis, neurofibromatosis, Parkinson's disease, paranoid psychoses, postherpetic neuralgia, schizophrenia, and Tourette's disorder; a reproductive disorder, such as a disorder of prolactin production, infertility, including tubal disease, ovulatory defects, and endometriosis, a disruption of the estrous cycle, a disruption of the menstrual cycle, polycystic ovary syndrome, ovarian hyperstimulation syndrome, an endometrial or ovarian tumor, a uterine fibroid, autoimmune disorders, an ectopic pregnancy, and teratogenesis; cancer of the breast, fibrocystic breast disease, and galactorrhea; a disruption of spermatogenesis, abnormal sperm physiology, cancer of the testis, cancer of the prostate, benign prostatic hyperplasia, prostatitis, Peyronie's disease, impotence, carcinoma of the male breast, and gynecomastia; and a cell proliferative disorder, such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, a cancer of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus. The polynucleotide sequences encoding SYNT may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and multiformat ELISA-like assays; and in microarrays utilizing fluids or tissues from patients to detect altered SYNT expression. Such qualitative or quantitative methods are well known in the art.

In a particular aspect, the nucleotide sequences encoding SYNT may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences encoding SYNT may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantified and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to

a control sample then the presence of altered levels of nucleotide sequences encoding SYNT in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

5 In order to provide a basis for the diagnosis of a disorder associated with expression of SYNT, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding SYNT, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from
10 normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used. Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

Once the presence of a disorder is established and a treatment protocol is initiated,
15 hybridization assays may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

With respect to cancer, the presence of an abnormal amount of transcript (either under- or
20 overexpressed) in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

25 Additional diagnostic uses for oligonucleotides designed from the sequences encoding SYNT may involve the use of PCR. These oligomers may be chemically synthesized, generated enzymatically, or produced in vitro. Oligomers will preferably contain a fragment of a polynucleotide encoding SYNT, or a fragment of a polynucleotide complementary to the polynucleotide encoding SYNT, and will be employed under optimized conditions for identification of a specific gene or
30 condition. Oligomers may also be employed under less stringent conditions for detection or quantification of closely related DNA or RNA sequences.

In a particular aspect, oligonucleotide primers derived from the polynucleotide sequences encoding SYNT may be used to detect single nucleotide polymorphisms (SNPs). SNPs are substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic
35 disease in humans. Methods of SNP detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and fluorescent SSCP (fSSCP) methods. In SSCP,

oligonucleotide primers derived from the polynucleotide sequences encoding SYNT are used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for example, from diseased or normal tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause differences in the secondary and tertiary structures of PCR products in single-stranded form, and these differences are detectable using gel electrophoresis in non-denaturing gels. In fSCCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis methods, termed in silico SNP (isSNP), are capable of identifying polymorphisms by comparing the sequence of individual overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass spectrometry using, for example, the high throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

Methods which may also be used to quantify the expression of SYNT include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) *J. Immunol. Methods* 159:235-244; Duplaa, C. et al. (1993) *Anal. Biochem.* 212:229-236.) The speed of quantitation of multiple samples may be accelerated by running the assay in a high-throughput format where the oligomer or polynucleotide of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as elements on a microarray. The microarray can be used in transcript imaging techniques which monitor the relative expression levels of large numbers of genes simultaneously as described in Seilhamer, J.J. et al., "Comparative Gene Transcript Analysis," U.S. Patent No. 5,840,484, incorporated herein by reference. The microarray may also be used to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, to monitor progression/regression of disease as a function of gene expression, and to develop and monitor the activities of therapeutic agents in the treatment of disease. In particular, this information may be used to develop a pharmacogenomic profile of a patient in order to select the most appropriate and effective treatment regimen for that patient. For example, therapeutic agents which are highly effective and display the fewest side effects may be selected for a patient based on his/her pharmacogenomic profile.

In another embodiment, antibodies specific for SYNT, or SYNT or fragments thereof may be used as elements on a microarray. The microarray may be used to monitor or measure protein-protein interactions, drug-target interactions, and gene expression profiles, as described above.

A particular embodiment relates to the use of the polynucleotides of the present invention to generate a transcript image of a tissue or cell type. A transcript image represents the global pattern of gene expression by a particular tissue or cell type. Global gene expression patterns are analyzed by quantifying the number of expressed genes and their relative abundance under given conditions and at a given time. (See Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, expressly incorporated by reference herein.) Thus a transcript image may be generated by hybridizing the polynucleotides of the present invention or their complements to the totality of transcripts or reverse transcripts of a particular tissue or cell type. In one embodiment, the hybridization takes place in high-throughput format, wherein the polynucleotides of the present invention or their complements comprise a subset of a plurality of elements on a microarray. The resultant transcript image would provide a profile of gene activity.

Transcript images may be generated using transcripts isolated from tissues, cell lines, biopsies, or other biological samples. The transcript image may thus reflect gene expression in vivo, as in the case of a tissue or biopsy sample, or in vitro, as in the case of a cell line.

Transcript images which profile the expression of the polynucleotides of the present invention may also be used in conjunction with in vitro model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental compounds. All compounds induce characteristic gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity (Nuwaysir, E.F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and N.L. Anderson (2000) Toxicol. Lett. 112-113:467-471, expressly incorporated by reference herein). If a test compound has a signature similar to that of a compound with known toxicity, it is likely to share those toxic properties. These fingerprints or signatures are most useful and refined when they contain expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality signature. Even genes whose expression is not altered by any tested compounds are important as well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization procedure is useful for comparison of expression data after treatment with different compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released February 29, 2000, available at <http://www.niehs.nih.gov/oc/news/toxchip.htm>.) Therefore, it is important and desirable in toxicological screening using toxicant signatures to include all expressed gene sequences.

In one embodiment, the toxicity of a test compound is assessed by treating a biological sample containing nucleic acids with the test compound. Nucleic acids that are expressed in the

treated biological sample are hybridized with one or more probes specific to the polynucleotides of the present invention, so that transcript levels corresponding to the polynucleotides of the present invention may be quantified. The transcript levels in the treated biological sample are compared with levels in an untreated biological sample. Differences in the transcript levels between the two samples are indicative of a toxic response caused by the test compound in the treated sample.

Another particular embodiment relates to the use of the polypeptide sequences of the present invention to analyze the proteome of a tissue or cell type. The term proteome refers to the global pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome can be subjected individually to further analysis. Proteome expression patterns, or profiles, are analyzed by quantifying the number of expressed proteins and their relative abundance under given conditions and at a given time. A profile of a cell's proteome may thus be generated by separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the separation is achieved using two-dimensional gel electrophoresis, in which proteins from a sample are separated by isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson, supra). The proteins are visualized in the gel as discrete and uniquely positioned spots, typically by staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical density of each protein spot is generally proportional to the level of the protein in the sample. The optical densities of equivalently positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are compared to identify any changes in protein spot density related to the treatment. The proteins in the spots are partially sequenced using, for example, standard methods employing chemical or enzymatic cleavage followed by mass spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of at least 5 contiguous amino acid residues, to the polypeptide sequences of the present invention. In some cases, further sequence data may be obtained for definitive protein identification.

A proteomic profile may also be generated using antibodies specific for SYNT to quantify the levels of SYNT expression. In one embodiment, the antibodies are used as elements on a microarray, and protein expression levels are quantified by exposing the microarray to the sample and detecting the levels of protein bound to each array element (Lueking, A. et al. (1999) Anal. Biochem. 270:103-111; Mendoze, L.G. et al. (1999) Biotechniques 27:778-788). Detection may be performed by a variety of methods known in the art, for example, by reacting the proteins in the sample with a thiol- or amino-reactive fluorescent compound and detecting the amount of fluorescence bound at each array element.

Toxicant signatures at the proteome level are also useful for toxicological screening, and should be analyzed in parallel with toxicant signatures at the transcript level. There is a poor

correlation between transcript and protein abundances for some proteins in some tissues (Anderson, N.L. and J. Seilhamer (1997) Electrophoresis 18:533-537), so proteome toxicant signatures may be useful in the analysis of compounds which do not significantly affect the transcript image, but which alter the proteomic profile. In addition, the analysis of transcripts in body fluids is difficult, due to rapid degradation of mRNA, so proteomic profiling may be more reliable and informative in such cases.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins that are expressed in the treated biological sample are separated so that the amount of each protein can be quantified. The amount of each protein is compared to the amount of the corresponding protein in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample. Individual proteins are identified by sequencing the amino acid residues of the individual proteins and comparing these partial sequences to the polypeptides of the present invention.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins from the biological sample are incubated with antibodies specific to the polypeptides of the present invention. The amount of protein recognized by the antibodies is quantified. The amount of protein in the treated biological sample is compared with the amount in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. USA 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.) Various types of microarrays are well known and thoroughly described in DNA Microarrays: A Practical Approach, M. Schena, ed. (1999) Oxford University Press, London, hereby expressly incorporated by reference.

In another embodiment of the invention, nucleic acid sequences encoding SYNT may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. Either coding or noncoding sequences may be used, and in some instances, noncoding sequences may be preferable over coding sequences. For example, conservation of a coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1

constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.) Once mapped, the nucleic acid sequences of the invention may be used to develop genetic linkage maps, for example, which correlate the inheritance of a disease state with the inheritance of a particular chromosome region or restriction fragment length polymorphism (RFLP). (See, e.g., Lander, E.S. and D. Botstein (1986) Proc. Natl. Acad. Sci. USA 83:7353-7357.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical and genetic map data. (See, e.g., Heinz-Ulrich, et al. (1995) in Meyers, supra, pp. 965-968.) Examples of genetic map data can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) World Wide Web site. Correlation between the location of the gene encoding SYNT on a physical map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder and thus may further positional cloning efforts.

In situ hybridization of chromosomal preparations and physical mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending genetic maps.

Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the exact chromosomal locus is not known. This information is valuable to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the gene or genes responsible for a disease or syndrome have been crudely localized by genetic linkage to a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequence of the instant invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier, or affected individuals.

In another embodiment of the invention, SYNT, its catalytic or immunogenic fragments, or oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes between SYNT and the agent being tested may be measured.

Another technique for drug screening provides for high throughput screening of compounds having suitable binding affinity to the protein of interest. (See, e.g., Geysen, et al. (1984) PCT application WO84/03564.) In this method, large numbers of different small test compounds are synthesized on a solid substrate. The test compounds are reacted with SYNT, or fragments thereof, and washed. Bound SYNT is then detected by methods well known in the art. Purified SYNT can also be coated directly onto plates for use in the aforementioned drug screening techniques.

Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding SYNT specifically compete with a test compound for binding SYNT. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with SYNT.

5 In additional embodiments, the nucleotide sequences which encode SYNT may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding
10 description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, in particular U.S. Ser. No. 60/144,992 and U.S. Ser. No. 60/168,858 are hereby expressly incorporated
15 by reference.

EXAMPLES

I. Construction of cDNA Libraries

RNA was purchased from Clontech or isolated from tissues described in Table 4. Some
20 tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

25 Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In some cases, RNA was treated with DNase. For most libraries, poly(A+) RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles (QIAGEN, Chatsworth CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA
30 purification kit (Ambion, Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene) or SUPERScript plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, supra, units
35 5.1-6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the

appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g.,

5 PBLUESCRIPT plasmid (Stratagene), PSPO1 plasmid (Life Technologies), pcDNA2.1 plasmid (Invitrogen, Carlsbad CA), or pINCY plasmid (Incyte Genomics, Palo Alto CA). Recombinant plasmids were transformed into competent *E. coli* cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectroMAX DH10B from Life Technologies.

II. Isolation of cDNA Clones

10 Plasmids obtained as described in Example I were recovered from host cells by *in vivo* excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8 Plus Plasmid, QIAWELL 8 Ultra Plasmid purification systems or the R.E.A.L. PREP 96

15 plasmid purification kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in

20 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Eugene OR) and a FLUOROSKAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

Incyte cDNA recovered in plasmids as described in Example II were sequenced as follows.

25 Sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 (PE Biosystems) thermal cyclor or the PTC-200 thermal cyclor (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific) or the MICROLAB 2200 (Hamilton) liquid transfer system. cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI

30 PRISM BIGDYE Terminator cycle sequencing ready reaction kit (PE Biosystems). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing system (PE Biosystems) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the

35 cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, *supra*, unit 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in

Example VI.

The polynucleotide sequences derived from cDNA sequencing were assembled and analyzed using a combination of software programs which utilize algorithms well known to those skilled in the art. Table 5 summarizes the tools, programs, and algorithms used and provides applicable

5 descriptions, references, and threshold parameters. The first column of Table 5 shows the tools, programs, and algorithms used, the second column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score, the
10 greater the homology between two sequences). Sequences were analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments were generated using the default parameters specified by the clustal algorithm as incorporated into the MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned
15 sequences.

The polynucleotide sequences were validated by removing vector, linker, and polyA sequences and by masking ambiguous bases, using algorithms and programs based on BLAST, dynamic programing, and dinucleotide nearest neighbor analysis. The sequences were then queried against a selection of public databases such as the GenBank primate, rodent, mammalian, vertebrate,
20 and eukaryote databases, and BLOCKS, PRINTS, DOMO, PRODOM, and PFAM to acquire annotation using programs based on BLAST, FASTA, and BLIMPS. The sequences were assembled into full length polynucleotide sequences using programs based on Phred, Phrap, and Consed, and were screened for open reading frames using programs based on GeneMark, BLAST, and FASTA. The full length polynucleotide sequences were translated to derive the corresponding full length
25 amino acid sequences, and these full length sequences were subsequently analyzed by querying against databases such as the GenBank databases (described above), SwissProt, BLOCKS, PRINTS, DOMO, PRODOM, Prosite, and Hidden Markov Model (HMM)-based protein family databases such as PFAM. HMM is a probabilistic approach which analyzes consensus primary structures of gene families. (See, e.g., Eddy, S.R. (1996) Curr. Opin. Struct. Biol. 6:361-365.)

30 The programs described above for the assembly and analysis of full length polynucleotide and amino acid sequences were also used to identify polynucleotide sequence fragments from SEQ ID NO:16-30. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies were described in The Invention section above.

IV. Analysis of Polynucleotide Expression

35 Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs

from a particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; Ausubel, 1995, supra, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in cDNA databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

$$\frac{\text{BLAST Score} \times \text{Percent Identity}}{5 \times \text{minimum} \{ \text{length}(\text{Seq. 1}), \text{length}(\text{Seq. 2}) \}}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. The product score is a normalized value between 0 and 100, and is calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the entire length of the shorter of the two sequences being compared. A product score of 70 is produced either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79% identity and 100% overlap.

The results of northern analyses are reported as a percentage distribution of libraries in which the transcript encoding SYNT occurred. Analysis involved the categorization of cDNA libraries by organ/tissue and disease. The organ/tissue categories included cardiovascular, dermatologic, developmental, endocrine, gastrointestinal, hematopoietic/immune, musculoskeletal, nervous, reproductive, and urologic. The disease/condition categories included cancer, inflammation, trauma, cell proliferation, neurological, and pooled. For each category, the number of libraries expressing the sequence of interest was counted and divided by the total number of libraries across all categories. Percentage values of tissue-specific and disease- or condition-specific expression are reported in Table 3.

V. Extension of SYNT Encoding Polynucleotides

The full length nucleic acid sequences of SEQ ID NO:16-30 were produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this fragment. One primer was synthesized to initiate 5' extension of the known fragment, and the other

primer, to initiate 3' extension of the known fragment. The initial primers were designed using OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

Selected human cDNA libraries were used to extend the sequence. If more than one extension was necessary or desired, additional or nested sets of primers were designed.

High fidelity amplification was obtained by PCR using methods well known in the art. PCR was performed in 96-well plates using the PTC-200 thermal cycler (MJ Research, Inc.). The reaction mix contained DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+} , $(NH_4)_2SO_4$, and β -mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ were as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well was determined by dispensing 100 μ l PICOGREEN quantitation reagent (0.25% (v/v) PICOGREEN; Molecular Probes, Eugene OR) dissolved in 1X TE and 0.5 μ l of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar, Acton MA), allowing the DNA to bind to the reagent. The plate was scanned in a Fluoroskan II (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 μ l to 10 μ l aliquot of the reaction mixture was analyzed by electrophoresis on a 1 % agarose mini-gel to determine which reactions were successful in extending the sequence.

The extended nucleotides were desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides were separated on low concentration (0.6 to 0.8%) agarose gels, fragments were excised, and agar digested with Agar ACE (Promega). Extended clones were religated using T4 ligase (New England Biolabs, Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent *E. coli* cells. Transformed cells were selected on antibiotic-containing media, and individual colonies were picked and cultured overnight at 37°C in 384-well plates in LB/2x carb liquid media.

The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase

(Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries were reamplified using the same conditions as described above. Samples were diluted with 20% dimethylsulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (PE Biosystems).

In like manner, the polynucleotide sequences of SEQ ID NO:16-30 are used to obtain 5' regulatory sequences using the procedure above, along with oligonucleotides designed for such extension, and an appropriate genomic library.

V. Chromosomal Mapping of SNYT Encoding Polynucleotides

The cDNA sequences which were used to assemble SEQ ID NO:16-30 were compared with sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these databases that matched SEQ ID NO:16-30 were assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as Phrap (Table 5). Radiation hybrid and genetic mapping data available from public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for Genome Research (WIGR), and Génethon were used to determine if any of the clustered sequences had been previously mapped. Inclusion of a mapped sequence in a cluster resulted in the assignment of all sequences of that cluster, including its particular SEQ ID NO., to that map location.

The genetic map locations of SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, and SEQ ID NO:30 are described in The Invention as ranges, or intervals, of human chromosomes. More than one map location is reported for SEQ ID NO:28 and SEQ ID NO:29, indicating that previously mapped sequences having similarity, but not complete identity, to SEQ ID NO:28 and SEQ ID NO:29 were assembled into their respective clusters. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Génethon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters. Diseases associated with the public and Incyte sequences located within the indicated intervals are also reported in the Invention where applicable. Human genome maps and other resources available to the public, such as the NCBI "GeneMap'99" World Wide Web site which can be accessed at <http://www.ncbi.nlm.nih.gov/genemap>, can be employed to determine if

previously identified disease genes map within or in proximity to the intervals indicated above.

VI. Labeling and Use of Individual Hybridization Probes

Hybridization probes derived from SEQ ID NO:16-30 are employed to screen cDNAs, genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 μ Ci of [γ - 32 P] adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech). An aliquot containing 10^7 counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under conditions of up to, for example, 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. Hybridization patterns are visualized using autoradiography or an alternative imaging means and compared.

VII. Microarrays

The linkage or synthesis of array elements upon a microarray can be achieved utilizing photolithography, piezoelectric printing (ink-jet printing, See, e.g., Baldeschweiler, supra), mechanical microspotting technologies, and derivatives thereof. The substrate in each of the aforementioned technologies should be uniform and solid with a non-porous surface (Skena (1999), supra). Suggested substrates include silicon, silica, glass slides, glass chips, and silicon wafers. Alternatively, a procedure analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be produced using available methods and machines well known to those of ordinary skill in the art and may contain any appropriate number of elements. (See, e.g., Skena, M. et al. (1995) Science 270:467-470; Shalon, D. et al. (1996) Genome Res. 6:639-645; Marshall, A. and J. Hodgson (1998) Nat. Biotechnol. 16:27-31.)

Full length cDNAs, Expressed Sequence Tags (ESTs), or fragments or oligomers thereof may comprise the elements of the microarray. Fragments or oligomers suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). The array elements are hybridized with polynucleotides in a biological sample. The polynucleotides in the biological sample are conjugated to a fluorescent label or other molecular tag for ease of detection.

After hybridization, nonhybridized nucleotides from the biological sample are removed, and a fluorescence scanner is used to detect hybridization at each array element. Alternatively, laser desorption and mass spectrometry may be used for detection of hybridization. The degree of complementarity and the relative abundance of each polynucleotide which hybridizes to an element on the microarray may be assessed. In one embodiment, microarray preparation and usage is described in detail below.

Tissue or Cell Sample Preparation

Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and poly(A)⁺ RNA is purified using the oligo-(dT) cellulose method. Each poly(A)⁺ RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/ μ l oligo-(dT) primer (21mer), 1X first strand buffer, 0.03 units/ μ l RNase inhibitor, 500 μ M dATP, 500 μ M dGTP, 500 μ M dTTP, 40 μ M dCTP, 40 μ M dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Pharmacia Biotech). The reverse transcription reaction is performed in a 25 ml volume containing 200 ng poly(A)⁺ RNA with GEMBRIGHT kits (Incyte). Specific control poly(A)⁺ RNAs are synthesized by *in vitro* transcription from non-coding yeast genomic DNA. After incubation at 37 °C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for 20 minutes at 85 °C to stop the reaction and degrade the RNA. Samples are purified using two successive CHROMA SPIN 30 gel filtration spin columns (CLONTECH Laboratories, Inc. (CLONTECH), Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The sample is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14 μ l 5X SSC/0.2% SDS.

Microarray Preparation

Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5 μ g. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Pharmacia Biotech).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR Scientific Products Corporation (VWR), West Chester PA), washed extensively in distilled water, and coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a 110°C oven.

Array elements are applied to the coated glass substrate using a procedure described in US

Patent No. 5,807,522, incorporated herein by reference. 1 μ l of the array element DNA, at an average concentration of 100 ng/ μ l, is loaded into the open capillary printing element by a high-speed robotic apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene).

- 5 Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate buffered saline (PBS) (Tropix, Inc., Bedford MA) for 30 minutes at 60 °C followed by washes in 0.2% SDS and distilled water as before.

Hybridization

- 10 Hybridization reactions contain 9 μ l of sample mixture consisting of 0.2 μ g each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The sample mixture is heated to 65 °C for 5 minutes and is aliquoted onto the microarray surface and covered with an 1.8 cm² coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly larger than a microscope slide. The chamber is kept at 100% humidity internally by the
15 addition of 140 μ l of 5X SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60 °C. The arrays are washed for 10 min at 45 °C in a first wash buffer (1X SSC, 0.1% SDS), three times for 10 minutes each at 45 °C in a second wash buffer (0.1X SSC), and dried.

Detection

- 20 Reporter-labeled hybridization complexes are detected with a microscope equipped with an Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-
25 scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a resolution of 20 micrometers.

- In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially. Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477, Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate
30 filters positioned between the array and the photomultiplier tubes are used to filter the signals. The emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source, although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

- The sensitivity of the scans is typically calibrated using the signal intensity generated by a
35 cDNA control species added to the sample mixture at a known concentration. A specific location on the array contains a complementary DNA sequence, allowing the intensity of the signal at that

location to be correlated with a weight ratio of hybridizing species of 1:100,000. When two samples from different sources (e.g., representing test and control cells), each labeled with a different fluorophore, are hybridized to a single array for the purpose of identifying genes that are differentially expressed, the calibration is done by labeling samples of the calibrating cDNA with the two fluorophores and adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital (A/D) conversion board (Analog Devices, Inc., Norwood MA) installed in an IBM-compatible PC computer. The digitized data are displayed as an image where the signal intensity is mapped using a linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping emission spectra) between the fluorophores using each fluorophore's emission spectrum.

A grid is superimposed over the fluorescence signal image such that the signal from each spot is centered in each element of the grid. The fluorescence signal within each element is then integrated to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte).

VIII. Complementary Polynucleotides

Sequences complementary to the SYNT-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring SYNT. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of SYNT. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the SYNT-encoding transcript.

IX. Expression of SYNT

Expression and purification of SYNT is achieved using bacterial or virus-based expression systems. For expression of SYNT in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac (tac)* hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express SYNT upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of SYNT in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus

(AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding SYNT by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945.)

In most expression systems, SYNT is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from SYNT at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, ch. 10 and 16). Purified SYNT obtained by these methods can be used directly in the assays shown in Examples X and XIV.

X. Demonstration of SYNT Activity

An SYNT activity assay measures aminoacylation of tRNA in the presence of a radiolabeled substrate. A cell-free extract depleted of endogenous aminoacyl-tRNA synthetase is prepared from Escherichia coli. SYNT, either biochemically purified or recombinantly produced, is added to the cell free extract. The cell-free extract is incubated with [¹⁴C]-labeled amino acid under conditions favorable for translation. Incorporation of the [¹⁴C]-labeled amino acid into acid-precipitable aminoacyl-tRNA is measured using a radioisotope counter. The amount of the [¹⁴C]-labeled amino acid incorporated into aminoacyl tRNA is proportional to the amount of SYNT activity. (See, for example, Ibba, M. et al. (1997) Science 278:1119-1122).

Alternatively, SYNT activity may be assayed as follows. SYNT, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent. (See, e.g., Bolton et al. (1973) Biochem. J. 133:529.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled SYNT, washed, and any wells with labeled SYNT complex are assayed. Data obtained using different concentrations of SYNT are used to calculate values for the number, affinity, and association of SYNT with the candidate molecules.

XI. Functional Assays

SYNT function is assessed by expressing the sequences encoding SYNT at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include pCMV SPORT plasmid (Life Technologies) and pCR3.1 plasmid (Invitrogen), both of which contain the cytomegalovirus promoter. 5-10 μ g of recombinant vector are transiently transfected into a human cell line, for example, an endothelial or hematopoietic cell line, using either liposome formulations or electroporation. 1-2 μ g of an additional plasmid containing sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M.G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of SYNT on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding SYNT and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding SYNT and other genes of interest can be analyzed by northern analysis or microarray techniques.

XII. Production of SYNT Specific Antibodies

SYNT substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the SYNT amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for

selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, *supra*, ch. 11.)

Typically, oligopeptides of about 15 residues in length are synthesized using an ABI 431A peptide synthesizer (PE Biosystems) using Fmoc chemistry and coupled to KLH (Sigma-Aldrich, St.

- 5 Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, 1995, *supra*.) Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide and anti-SYNT activity by, for example, binding the peptide or SYNT to a substrate, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

10 **XIII. Purification of Naturally Occurring SYNT Using Specific Antibodies**

- Naturally occurring or recombinant SYNT is substantially purified by immunoaffinity chromatography using antibodies specific for SYNT. An immunoaffinity column is constructed by covalently coupling anti-SYNT antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is
15 blocked and washed according to the manufacturer's instructions.

- Media containing SYNT are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of SYNT (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/SYNT binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such
20 as urea or thiocyanate ion), and SYNT is collected.

XIV. Identification of Molecules Which Interact with SYNT

- SYNT, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent. (See, e.g., Bolton A.E. and W.M. Hunter (1973) *Biochem. J.* 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled SYNT, washed,
25 and any wells with labeled SYNT complex are assayed. Data obtained using different concentrations of SYNT are used to calculate values for the number, affinity, and association of SYNT with the candidate molecules.

- Alternatively, molecules interacting with SYNT are analyzed using the yeast two-hybrid system as described in Fields, S. and O. Song (1989, *Nature* 340:245-246), or using commercially
30 available kits based on the two-hybrid system, such as the MATCHMAKER system (Clontech).

SYNT may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT) which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent No. 6,057,101).

35

Various modifications and variations of the described methods and systems of the invention

will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with certain embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention

5 which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

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Table 1

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
1	16	1806212	SINTNOT13	268731R1 (HNT2NOT01), 410547R1 (BRSTNOT01), 642383F1 (BRSTNOT03), 642383R6 (BRSTNOT03), 1484778F6 (CORPNOT02), 1577276X13 (LNODNOT03), 1577276X14 (LNODNOT03), 1577276X16 (LNODNOT03), 1733808F6 (BRSTNOT08), 2057185R6 (BEPINOT01), 1308705F1 (COLNFET02), 1337653F1 (COLNNOT13), 1430326F1 (SINTBST01), 1525049F6 (UCMCL5T01), 1525049T7 (UCMCL5T01), 1807032F6 (SINTNOT13), 2083883X31C1 (UTRSNOT08), 20838831X54C1, SAEA01919R1, SAEA00070F1
2	17	2083883	UTRSNOT08	1334395F6 (COLNNOT13), 1607276F6 (LUNGNOT15), 1930074F6 (COLNTUT03), 1978977R6 (LUNGNOT03), 2054860R6 (BEPINOT01), 2454288H1 (ENDANOT01), 2791177H2 (COLNTUT16), 4049241H1 (SINTNOT18), 4787755H1 (BRATNOT03)
3	18	2454288	ENDANOT01	285705F1 (EOSIHET02), 515506F1 (MMLR1DT01), 515506R1 (MMLR1DT01), 723201R1 (SYNOOAT01), 726178R1 (SYNOOAT01), 906091R1 (COLNNOT08), 1492309T1 (PROSNON01), 1513539H1 (PANCUTUT01), 2632033H1 (COLNTUT15)
4	19	1513539	PANCUTUT01	655968H1 (EOSINOT03), 820407T1 (KERANOT02), 1383948F1 (BRAITUT08), 1383996T6 (BRAITUT08), 1441048R1 (THYRNOT03), 1579330F6 (DUODNOT01), 2148623H1 (BRAINOT09), 3170589H1 (BRSTNOT18), 3251591H1 (SEMVNOT03), 3618285H1 (EPIFNOT01), 3637486H1 (LUNGNOT30), g1524807
5	20	2148623	BRAINOT09	2457R1 (U937NOT01), 270182R1 (HNT2NOT01), 730115H1 (LUNGNOT03), 991450H1 (COLNNOT11), 994055T1 (COLNNOT11), 1308496H1 (COLNFET02), 1808269F6 (SINTNOT13), 1875536T6 (LEUKNOT02), 1978055H1 (LUNGNOT03), 2579405H1 (KIDNTUT13), 2583944H1 (BRAITUT22)
6	21	2579405	KIDNTUT13	283147F1 (CARDNOT01), 904594R2 (COLNNOT07), 2662427H1 (ADRENOT08), 2860066H1 (SININOT03), 3078653H1 (BRAITUT01), 3852430F6 (BRAITUT12), 3852430T6 (BRAITUT12), SCDA09024V1, SCDA05143V1
7	22	2662427	ADRENOT08	

Table 1 (cont.)

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
8	23	2844928	DRGLNOT01	1466601F1 (PANCTUT02), 1662986F6 (BRSTNOT09), 1732880F6 (BRSTTUT08), 1804107F6 (SINTNOT13), 2521851F6 (BRAITUT21), 2662837X303B1 (ADRENOT08), 2844928H1 (DRGLNOT01), 2967532H1 (SCORNOT04), 3774082H1 (BRSTNOT25), 5871970H1 (COLTDIT04)
9	24	3231586	COTRNOT01	319277H1 (EOSTHET02), 920940H1 (RATRNOT02), 1445995H1 (PLACNOT02), 1517438F1 (PANCTUT01), 1963042H1 (BRSTNOT04), 2023159H1 (CONNNOT01), 2932203H1 (UTRSNOR01), 3231586H1 (COTRNOT01), 3346128H1 (BRAITUT24), g1474393
10	25	3580770	293TF3T01	269986R1 (HNT2NOT01), 269986R6 (HNT2NOT01), 3580770H1 (293TF3T01), 3602575F6 (DRGTNOT01), 3602575T6 (DRGTNOT01), g1839725
11	26	3778612	BRSTNOT27	3778612F6 (BRSTNOT27), 3778612H1 (BRSTNOT27), 4063060T6 (BRAINOT21)
12	27	4574912	PROSTMT02	224714F1 (PANCTUT01), 452757F1 (TYLMNOT02), 1210705R7 (BRSTNOT02), 1437821F6 (PANCTUT08), 2700694F6 (OVARUT10), 3963634H1 (PROSNOT14), 3964731H1 (PROSNOT14), 4574912H1 (PROSTMT02), 5035739H1 (LIVRTUT13)
13	28	5630806	PLACFER01	1649584X20C1 (PROSTUT09), 1649855X12C1 (PROSTUT09), 1650519X14C1 (PROSTUT09), 2054061R6 (BEPINOT01), 2347805X304V1 (COLSUCT01), 3384595H1 (ESOGNOT04), 5630806H1 (PLACFER01)
14	29	5854855	FIBAUNT02	746434R1 (BRAITUT01), 815240R1 (OVARUT01), 2515988F6 (LIVRTUT04), 3105953F6 (BRSTTUT15), 5854855H1 (FIBAUNT02)
15	30	5993973	FTUBTUT02	270363H1 (HNT2NOT01), 1863382F6 (PROSNOT19), 2696339F6 (UTRSNOR12), 3500696H1 (PROSTUT13), 4247086H1 (BRABDIT01), 5195020H1 (LUNLTUT04), 5591818H1 (COLCDIT03), 6023466H1 (TESTNOT11)

Table 2

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosyla- tion Sites	Signature Sequences, Motifs, and Domains	Homologous Sequences	Analytical Methods and Databases
1	1176	T7 T238 T543 S35 S68 S167 S175 T224 S241 T379 S396 T444 S453 S518 T552 S593 S673 T749 T769 T791 S978 S1042 T1083 T26 T41 S128 S153 T293 T327 S368 T557 S697 S714 S783 T925 S1082 T1136 S1153 Y111 Y666	N33 N333 N439 N882	Leucine-tRNA ligase domain T303-I870 Amino-transfer RNA synthetase N36-F88 N713-N723	similar to leucyl-tRNA synthetase [Arabidopsis thaliana] g2160156	MOTIFS BLAST-GenBank BLAST-DOMO PROFILES-SCAN BLAST-PRODOME BLIMPS-BLOCKS
2	739	S28 T132 S185 S282 S288 S307 T320 T352 S451 S661 T728 S732 S116 S163 S168 S261 T398 S436 T590 S633 T714 Y173 Y349 Y725 Y734	N102 N588 N619	AMP-binding domain S163-V629, N294-V345 E309-I320, T321-I329 Long-chain acyl-CoA synthetase P158-E280	fatty acid coenzyme A ligase 5 [Homo sapiens] g6174680	MOTIFS BLAST-GenBank BLAST-DOMO PROFILES-SCAN BLAST-PRODOME BLIMPS-BLOCKS HMMER-PFAM BLIMPS-PRINTS
3	589	S179 T18 T20 S40 S138 T193 T256 T298 T354 S419 S485 T570 S579 S5 T114 T174	N187	Phenylalanyl-tRNA synthetase P2-Q556, N293-L589 Synthetase b chain D59-L84, R355-Y374 I439-N465	phenylalanyl tRNA synthetase beta subunit [M. musculus] g4633656	MOTIFS BLAST-GenBank BLAST-PRODOME BLIMPS-PRODOME

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosyla- tion Sites	Signature Sequences, Motifs, and Domains	Homologous Sequences	Analytical Methods and Databases
4	157	S26 S69 T131 T132 S108	N18	Signal peptide: M1-V66 Acetyl-CoA carboxylase carboxyl transferase alpha subunit signature: G128-I139	acetyl- coenzyme A synthetase [Penicillium chrysogenum] g265229	BLAST-GenBank SPSCAN BLOCKS-PRINTS MOTIFS
5	643	T308 T337 S402 S433 T454 S34 S101 T408 S530 S621	N9 N33 N90 N104 N259 N306 N431 N571 N634	Class II glutamine amidotransferase motif: L27-K36, G545-F560 (p<0.01) Transferase/ligase motif: R30-A224, S258-F356, P404-Q484	putative asparagine synthase [S. pombe] g3560144	BLAST-GenBank BLIMPS-BLOCKS BLAST-PRODOM MOTIFS
6	660	T282 S315 S329 T487 T596 S9 S276 T459 T624 Y230	N140	Class-I aminoacyl-tRNA synthetase signature: I74-M660, V183-L233, P201-L212, S519-N529 Arg-tRNA synthetase: K193-L224, V232-F245, T374-R395, H237-M660, S78-M660	arginyl-tRNA synthetase, ArgRS [Homo sapiens] g1217668	BLAST-GenBank HMMER-PFAM BLIMPS-BLOCKS PROFILES SCAN BLIMPS-PFAM BLAST-PRODOM BLAST-DOMO MOTIFS

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosyla- tion Sites	Signature Sequences, Motifs, and Domains	Homologous Sequences	Analytical Methods and Databases
7	725	S723 S80 S220 S238 T351 S371 T414 T465 S591 S641 T38 T45 T67 T165 S230 T252 T407 S413 S454 S499 S541 T554 T685 S688 T693 S719	N48 N472 N546 N552	Biotin-requiring enzyme signature: P652-F714, I657-R707 Biotin attachment site: K681 Acetyl-CoA biotin carboxyl carrier protein signature: F661-M675, V676-P689 Carbamoyl-PO4 synthase signature: K51-P490, E193-K494, F333-L340, L245-P290, Y270-K494, F331-G365	3-methyl- crotonyl CoA carboxylase homolog [C. elegans] g3876562	BLAST-GenBank HMMER-PFAM BLIMPS-BLOCKS PROFILES-SCAN BLIMPS-PRINTS BLAST-PRODOM BLAST-DOMO MOTIFS
8	644	S30 S253 S370 T457 T496 T593 T594 S43 T65 S207 S237 S269 S626 Y247 Y521	N282	AMP-binding domain signature: E79-V538, T101-V540, S240-L293, H255-L275, F262-H277, I260-K271, V570-R635 Ligase/synthetase signature: T356-R640	predicted long chain fatty acid CoA ligase [C. elegans] g4262587	BLAST-GenBank HMMER-PFAM BLIMPS-BLOCKS PROFILES-SCAN BLIMPS-PRINTS BLAST-PRODOM BLAST-DOMO MOTIFS
9	504	S122 S134 S428 S111 T349	N9 N39 N209 N426	Signal peptide: M1-A67 Aminotransferase class- II pyridoxal-PO4 attachment site: A104-R113		SPSCAN BLIMPS-BLOCKS MOTIFS

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosyla- tion Sites	Signature Sequences, Motifs, and Domains	Homologous Sequences	Analytical Methods and Databases
10	489	S51 T150 T220 S465 S477 T90 S200 T250 T350 S433 S467 Y83		RNA methyl transferase SpoU family: P344-G354 CTP synthetase domain: K2-N455, M1-Y457, M335-Y457	CTP synthetase homolog (CTPsh) [Mus musculus] g1654185	BLAST-GenBank BLIMPS-PFAM BLAST-PRODOM BLAST-DOMO MOTIFS
11	258	S105 S115 S139		Signal peptide: M1-G43 ATP synthase signature: Y98-L129 S-adenosyl methionine synthetase signature: A209-V257		SPSCAN HMMER-PFAM PROFILESCAN MOTIFS
12	555	S22 T72 T110 S132 S165 S190 S258 S342 S363 S446 S539 S31 T179 S212 S312 T318 S339 S380 S392 T393 T407 S428 T519 Y24		Aminoacyl tRNA synthetase signature: V73-A82, K305-N315 (p<1.1e-3) Cysteinylyl-tRNA synthetase signature: R66-A77, I103-V112, E230-C248, D261-E282, Y67-E282, H76-A494	putative cysteinylyl- tRNA synthetase [S. pombe] g1044932	BLAST-GenBank BLIMPS-BLOCKS BLIMPS-PRINTS BLAST-PRODOM BLAST-DOMO MOTIFS
13	463	S54 S79 S124 S235 T253 T295 T411 T15 S366 Y84	N52	Succinyl-CoA ligase family: I97-F111, V181-E193, L314-A343, L53-D367, D290-K442, L53-I463	ATP-specific succinyl-CoA synthetase beta subunit [Homo sapiens] g3766196	BLAST-GenBank BLIMPS-BLOCKS BLAST-PRODOM BLAST-DOMO MOTIFS

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosyla- tion Sites	Signature Sequences, Motifs, and Domains	Homologous Sequences	Analytical Methods and Databases
14	399	T151 S179 S19 S72 T95 T151 S157 S191 S192 T217 T218 S260 T318 S337 S353		Signal peptide: M1-G42 Class-I aminoacyl-tRNA synthetase signature: P54-L64		SPSCAN MOTIFS
15	339	S187 T232 T266 S9 S31 T221 T231 S274 S276 T278 S324 S31 S36 T78 S223 S317 Y265		Phenylalanyl-tRNA synthetase family: V81-E261	similar to phenylalanyl- tRNA synthetase [C. elegans] g3876233	BLAST-GenBank BLAST-PRODOM MOTIFS

Table 3

Nucleotide SEQ ID NO:	Selected Fragments	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
16	153-197 600-644 1198-2042	Nervous (0.240) Reproductive (0.231) Hematopoietic/Immune (0.124)	Cancer (0.488) Inflammation/Trauma (0.306) Cell proliferation (0.198)	pINCY
17	163-207 1090-1134	Gastrointestinal (0.333) Reproductive (0.205) Hematopoietic/Immune (0.141)	Cancer (0.462) Inflammation/Trauma (0.372) Cell proliferation (0.103)	pINCY
18	601-645	Reproductive (0.216) Gastrointestinal (0.205) Nervous (0.148)	Cancer (0.477) Inflammation/Trauma (0.330) Cell proliferation (0.227)	PBLUESCRIPT
19	1-531 1634-2122	Reproductive (0.224) Nervous (0.165) Gastrointestinal (0.153)	Cancer (0.365) Inflammation (0.282) Cell proliferation (0.176)	pINCY
20	345-418 1272-1762 2039-2357	Cardiovascular (0.194) Reproductive (0.181) Nervous (0.153)	Cancer (0.514) Cell proliferation (0.194) Inflammation (0.181)	pINCY
21	1-109	Gastrointestinal (0.175) Nervous (0.175) Reproductive (0.175)	Cancer (0.427) Inflammation (0.252) Cell proliferation (0.243)	pINCY
22	2045-2317	Nervous (0.232) Reproductive (0.214) Cardiovascular (0.179)	Cancer (0.411) Inflammation (0.268) Trauma (0.161)	pINCY
23	1-508, 840-1183 1656-1741 1968-2254	Reproductive (0.266) Nervous (0.188) Endocrine (0.125)	Cancer (0.578) Inflammation (0.234) Cell proliferation (0.125)	pINCY
24		Reproductive (0.315) Gastrointestinal (0.150) Hematopoietic/Immune (0.150)	Cancer (0.433) Inflammation (0.283) Cell proliferation (0.126)	pINCY
25	1-151	Reproductive (0.333) Nervous (0.250) Hematopoietic (0.167)	Cancer (0.583) Inflammation (0.333) Cell proliferation (0.167)	pINCY

Table 3 (cont.)

Nucleotide SEQ ID NO:	Selected Fragments	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
26	1-214 567-970	Nervous (0.286) Reproductive (0.286) Cardiovascular (0.143) Endocrine (0.143)	Cancer (0.524) Inflammation (0.190) Trauma (0.190)	pINCY
27	1-206 1129-1206	Reproductive (0.243) Hematopoietic/Immune (0.143) Cardiovascular (0.129) Gastrointestinal (0.129) Nervous (0.129)	Cancer (0.457) Cell proliferation (0.229) Inflammation (0.186)	pINCY
28		Nervous (0.238) Gastrointestinal (0.190) Reproductive (0.190)	Cancer (0.429) Inflammation (0.274) Cell proliferation (0.131)	pINCY
29	1-234 1229-1477	Reproductive (0.331) Nervous (0.204) Gastrointestinal (0.116)	Cancer (0.508) Cell proliferation (0.188) Inflammation (0.182)	pINCY
30	1-871 1026-1138 1356-1660	Reproductive (0.378) Nervous (0.162) Gastrointestinal (0.135)	Cancer (0.649) Cell proliferation (0.189) Inflammation (0.189)	pINCY

Table 4

Nucleotide SEQ ID NO:	Library	Library Description
16	SINTNOT13	Library was constructed using RNA isolated from ileum tissue obtained from a 25-year-old Asian female during a partial colectomy and temporary ileostomy. Pathology indicated moderately active chronic ulcerative colitis, involving colonic mucosa from the distal margin to the ascending colon. Family history included hyperlipidemia, malignant cervical neoplasm, viral hepatitis A, and depressive disorder.
17	UTRENOT08	Library was constructed using RNA isolated from uterine tissue removed from a 35-year-old Caucasian female during a vaginal hysterectomy with dilation and curettage. Pathology indicated that the endometrium was secretory phase with a benign endometrial polyp 1 cm in diameter. The cervix showed mild chronic cervicitis. Family history included atherosclerotic coronary artery disease and type II diabetes.
18	ENDANOT01	Library was constructed using RNA isolated from aortic endothelial cell tissue from an explanted heart removed from a male during a heart transplant.
19	PANCTUT01	This library was constructed using RNA isolated from pancreatic tumor tissue removed from a 65-year-old Caucasian female. Pathology indicated invasive adenocarcinoma. Patient history included type II diabetes, osteoarthritis, cardiovascular disease, benign neoplasm in the large bowel, and a cataract. Family history included cardiovascular disease, type II diabetes, and stomach cancer.
20	BRAINOT09	This library was constructed using RNA isolated from brain tissue removed from a Caucasian male fetus, who died at 23 weeks' gestation.
21	KIDNTUT13	This library was constructed using RNA isolated from kidney tumor tissue removed from a 51-year-old Caucasian female. Pathology indicated renal cell carcinoma. Patient history included depressive disorder, hypoglycemia, and uterine endometriosis. Family history included calculus of the kidney, colon cancer, and type II diabetes.
22	ADRENOT08	This library was constructed using RNA isolated from adrenal tissue removed from a 20-year-old Caucasian male, who died from head trauma.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
23	DRGLNOT01	This library was constructed using RNA isolated from dorsal root ganglion tissue removed from the low thoracic/high lumbar region of a 32-year-old Caucasian male who died from acute pulmonary edema and bronchopneumonia, bilateral pleural and pericardial effusions, and malignant lymphoma (natural killer cell type). Patient history included probable cytomegalovirus infection, hepatic congestion and steatosis, splenomegaly, hemorrhagic cystitis, thyroid hemorrhage, and Bell's palsy. Treatment included radiation therapy.
24	COTRNOT01	This library was constructed using RNA isolated from diseased transverse colon tissue obtained from a 26-year-old Caucasian male. Pathology indicated minimally active pancolitis with areas of focal severe colitis with perforation, consistent with Crohn's disease.
25	293TF3T01	This library was constructed using RNA isolated from a serum-starved transformed embryonal cell line (293-EBNA) derived from kidney epithelial tissue. The cells were transformed with adenovirus 5 DNA.
26	BRSTNOT27	This library was constructed using RNA isolated from breast tissue removed from a 57-year-old Caucasian female. Pathology for the associated tumor tissue indicated residual micro-scopic infiltrating adenocarcinoma and extensive intraductal carcinoma. Immunoperoxidase stains for estrogen and progesterone receptors were positive. Patient history included benign hypertension, hyperlipidemia, cardiac dysrhythmia, a benign colon neoplasm, a solitary breast cyst, and a breast neoplasm. Family history included benign hypertension, acute leukemia, primary liver cancer, and lung cancer.
27	PROSTM02	This library was constructed using RNA isolated from diseased prostate tissue removed from a 66-year-old Caucasian male. Pathology indicated adenofibromatous hyperplasia. Pathology from the associated tumor indicated adenocarcinoma. The patient presented with elevated prostate specific antigen (PSA) and induration. Family history included acute myocardial infarction, atherosclerotic coronary artery disease, type II diabetes, hyperlipidemia, and Jakob-Creutzfeldt disease.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
28	PLACFER01	This library was constructed from RNA isolated from placental tissue from a Caucasian fetus, who died at 16 weeks' gestation from fetal demise and hydrocephalus. Patient history included umbilical cord wrapped around the head and shoulders. Serology was positive for anti-CMV. Family history included multiple pregnancies and live births, and an abortion.
29	FIBAUNT02	This library was constructed using RNA isolated from untreated aortic adventitial fibroblasts removed from a 65-year-old Caucasian female.
30	FTUBTUT02	This library was constructed using RNA isolated from fallopian tube tumor tissue removed from an 85-year-old Caucasian female. Pathology indicated poorly differentiated mixed endometrioid and serous adenocarcinoma. Pathology for the associated uterus tumor indicated focal and metastatic endometrioid adenocarcinoma and moderately differentiated invasive adenocarcinoma. Patient history included medullary carcinoma of the thyroid and myocardial infarction.

Table 5

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	PE Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	PE Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	PE Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25:3389-3402.	ESTs: Probability value= 1.0E-8 or less Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad. Sci. USA 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183:63-98; and Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value=1.06E-6 Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater fastx E value=1.0E-8 or less Full Length sequences: fastx score=100 or greater
BLIMPS	A BLOCKS IMPROVED Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) Nucleic Acids Res. 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37:417-424.	Score=1000 or greater; Ratio of Score/Strength = 0.75 or larger; and, if applicable, Probability value= 1.0E-3 or less
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) J. Mol. Biol. 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322.	Score=10-50 bits for PFAM hits, depending on individual protein families

Table 5 (cont.)

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribkov, M. et al. (1988) CABIOS 4:61-66; Gribkov, M. et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221.	Normalized quality score \geq GCG-specified "HIGH" value for that particular Prosite motif. Generally, score=1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M.S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12:431-439.	Score=3.5 or greater
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

What is claimed is:

1. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

- 5 a) an amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14,
- b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14,
- 10 c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, and
- 15 d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14.

20

2. An isolated polypeptide of claim 1 selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14.

25

3. An isolated polynucleotide encoding a polypeptide of claim 1.

4. An isolated polynucleotide encoding a polypeptide of claim 2.

5. An isolated polynucleotide of claim 4 selected from the group consisting of SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29.

30

6. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 3.

35

7. A cell transformed with a recombinant polynucleotide of claim 6.
8. A transgenic organism comprising a recombinant polynucleotide of claim 6.
- 5 9. A method for producing a polypeptide of claim 1, the method comprising:
- a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide encoding the polypeptide of claim 1, and
- 10 b) recovering the polypeptide so expressed.
10. An isolated antibody which specifically binds to a polypeptide of claim 1.
11. An isolated polynucleotide comprising a polynucleotide sequence selected from the
- 15 group consisting of:
- a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29,
- b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a
- 20 polynucleotide sequence selected from the group consisting of SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29,
- c) a polynucleotide sequence complementary to a),
- d) a polynucleotide sequence complementary to b), and
- 25 e) an RNA equivalent of a)-d).
12. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 11.
13. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:
- a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization
- 35 complex is formed between said probe and said target polynucleotide or fragments thereof, and
- b) detecting the presence or absence of said hybridization complex, and, optionally, if

present, the amount thereof.

14. A method of claim 13, wherein the probe comprises at least 60 contiguous nucleotides.

5 15. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:

a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and

10 b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

16. A composition comprising an effective amount of a polypeptide of claim 1 and a pharmaceutically acceptable excipient.

15 17. A composition of claim 16, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14.

20 18. A method for treating a disease or condition associated with decreased expression of functional SYNT, comprising administering to a patient in need of such treatment the composition of claim 16.

25 19. A method for screening a compound for effectiveness as an agonist of a polypeptide of claim 1, the method comprising:

a) exposing a sample comprising a polypeptide of claim 1 to a compound, and

b) detecting agonist activity in the sample.

30 20. A composition comprising an agonist compound identified by a method of claim 19 and a pharmaceutically acceptable excipient.

21. A method for treating a disease or condition associated with decreased expression of functional SYNT, comprising administering to a patient in need of such treatment a pharmaceutical composition of claim 20.

35 22. A method for screening a compound for effectiveness as an antagonist of a polypeptide

of claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting antagonist activity in the sample.

5 23. A composition comprising an antagonist compound identified by a method of claim 22 and a pharmaceutically acceptable excipient.

 24. A method for treating a disease or condition associated with overexpression of functional SYNT, comprising administering to a patient in need of such treatment a composition of claim 23.

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 25. A method of screening for a compound that specifically binds to the polypeptide of claim 1, said method comprising the steps of:

 a) combining the polypeptide of claim 1 with at least one test compound under suitable conditions, and

15

 b) detecting binding of the polypeptide of claim 1 to the test compound, thereby identifying a compound that specifically binds to the polypeptide of claim 1.

 26. A method of screening for a compound that modulates the activity of the polypeptide of claim 1, said method comprising:

20

 a) combining the polypeptide of claim 1 with at least one test compound under conditions permissive for the activity of the polypeptide of claim 1,

 b) assessing the activity of the polypeptide of claim 1 in the presence of the test compound, and

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 c) comparing the activity of the polypeptide of claim 1 in the presence of the test compound with the activity of the polypeptide of claim 1 in the absence of the test compound, wherein a change in the activity of the polypeptide of claim 1 in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide of claim 1.

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 27. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 5, the method comprising:

- a) exposing a sample comprising the target polynucleotide to a compound, and
- b) detecting altered expression of the target polynucleotide.

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 28. A method for assessing toxicity of a test compound, said method comprising:

- a) treating a biological sample containing nucleic acids with the test compound;

- b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 11 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim
- 5 11 or fragment thereof;
- c) quantifying the amount of hybridization complex; and
- d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test
- 10 compound.

**DECLARATION AND POWER OF ATTORNEY FOR
UNITED STATES PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,
and

I believe that I am the original, first and sole inventor (if only one name is listed below)
or an original, first and joint inventor (if more than one name is listed below) of the subject
matter which is claimed and for which a United States patent is sought on the invention entitled

HUMAN SYNTHETASES

the specification of which:

 / is attached hereto.

 / was filed on _____ as application Serial No. _____ and if this box
contains an X /, was amended on _____.

 X / was filed as Patent Cooperation Treaty international application No. PCT/US00/19980 on
July 20, 2000, if this box contains an X /, was amended on under Patent Cooperation Treaty
Article 19 on _____, and if this box contains an X /, was amended on _____.

I hereby state that I have reviewed and understand the contents of the above-identified
specification, including the claims, as amended by any amendment referred to above.

I acknowledge my duty to disclose information which is material to the examination of
this application in accordance with Title 37, Code of Federal Regulations, §1.56(a).

I hereby claim the benefit under Title 35, United States Code, §119 or §365(a)-(b) of any
foreign application(s) for patent or inventor's certificate indicated below and of any Patent
Cooperation Treaty international applications(s) designating at least one country other than the
United States indicated below and have also identified below any foreign application(s) for
patent or inventor's certificate and Patent Cooperation Treaty international application(s)
designating at least one country other than the United States for the same subject matter and
having a filing date before that of the application for said subject matter the priority of which is
claimed:

Country	Number	Filing Date	Priority Claimed
_____	_____	_____	// Yes // No
_____	_____	_____	// Yes // No

I hereby claim the benefit under Title 35, United States Code, §119(e) of any United States provisional application(s) listed below.

Application Serial No.	Filed	Status (Pending, Abandoned, Patented)
60/144,992	July 22, 1999	Expired
60/168,858	December 2, 1999	Expired

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in said prior application(s) in the manner required by the first paragraph of Title 35, United States Code §112, I acknowledge my duty to disclose material information as defined in Title 37 Code of Federal Regulations, §1.56(a) which occurred between the filing date(s) of the prior application(s) and the national or Patent Cooperation Treaty international filing date of this application:

Application Serial No.	Filed	Status (Pending, Abandoned, Patented)
_____	_____	_____

I hereby appoint the following:

Lucy J. Billings	Reg. No. 36,749
Michael C. Cerrone	Reg. No. 39,132
Diana Hamlet-Cox	Reg. No. 33,302
Richard C. Ekstrom	Reg. No. 37,027
Barrie D. Greene	Reg. No. 46,740
Matthew R. Kaser	Reg. No. 44,817
Lynn E. Murry	Reg. No. 42,918
Shirley A. Recipon	Reg. No. 47,016
Susan K. Sather	Reg. No. 44,316
Michelle M. Stempien	Reg. No. 41,327
David G. Streeter	Reg. No. 43,168
Stephen Todd	Reg. No. 47,139
P. Ben Wang	Reg. No. 41,420

respectively and individually, as my patent attorneys and/or agents, with full power of substitution and revocation, to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith. Please address all communications to:

**LEGAL DEPARTMENT
INCYTE GENOMICS, INC.
3160 PORTER DRIVE, PALO ALTO, CA 94304**

TEL: 650-855-0555 FAX: 650-849-8886 or 650-845-4166

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

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Second Joint Inventor:

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Date: _____, 2001

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Ninth Joint Inventor:

Full name: Yalda Azimzai

Signature: _____

Date: _____, 2001

Citizenship: United States

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P.O. Address: 5518 Boulder Canyon Drive
Castro Valley, California 94552

2025-06-10 10:10:10

**DECLARATION AND POWER OF ATTORNEY FOR
UNITED STATES PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,
and

I believe that I am the original, first and sole inventor (if only one name is listed below)
or an original, first and joint inventor (if more than one name is listed below) of the subject
matter which is claimed and for which a United States patent is sought on the invention entitled

HUMAN SYNTHETASES

the specification of which:

 / / is attached hereto.

 / was filed on _____ as application Serial No. _____ and if this box
contains an X / /, was amended on _____.

 / / was filed as Patent Cooperation Treaty international application No. PCT/US00/19980 on
July 20, 2000, if this box contains an X / /, was amended on under Patent Cooperation Treaty
Article 19 on _____, and if this box contains an X / /, was amended on _____.

I hereby state that I have reviewed and understand the contents of the above-identified
specification, including the claims, as amended by any amendment referred to above.

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this application in accordance with Title 37, Code of Federal Regulations, §1.56(a).

I hereby claim the benefit under Title 35, United States Code, §119 or §365(a)-(b) of any
foreign application(s) for patent or inventor's certificate indicated below and of any Patent
Cooperation Treaty international applications(s) designating at least one country other than the
United States indicated below and have also identified below any foreign application(s) for
patent or inventor's certificate and Patent Cooperation Treaty international application(s)
designating at least one country other than the United States for the same subject matter and
having a filing date before that of the application for said subject matter the priority of which is
claimed:

Country	Number	Filing Date	Priority Claimed
_____	_____	_____	// Yes // No
_____	_____	_____	// Yes // No

I hereby claim the benefit under Title 35, United States Code, §119(e) of any United States provisional application(s) listed below.

Application Serial No.	Filed	Status (Pending, Abandoned, Patented)
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60/168,858	December 2, 1999	Expired

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in said prior application(s) in the manner required by the first paragraph of Title 35, United States Code §112, I acknowledge my duty to disclose material information as defined in Title 37 Code of Federal Regulations, §1.56(a) which occurred between the filing date(s) of the prior application(s) and the national or Patent Cooperation Treaty international filing date of this application:

Application Serial No.	Filed	Status (Pending, Abandoned, Patented)
_____	_____	_____

I hereby appoint the following:

Lucy J. Billings	Reg. No. <u>36,749</u>
Michael C. Cerrone	Reg. No. <u>39,132</u>
Diana Hamlet-Cox	Reg. No. <u>33,302</u>
Richard C. Ekstrom	Reg. No. <u>37,027</u>
Barrie D. Greene	Reg. No. <u>46,740</u>
Matthew R. Kaser	Reg. No. <u>44,817</u>
Lynn E. Murry	Reg. No. <u>42,918</u>
Shirley A. Recipon	Reg. No. <u>47,016</u>
Susan K. Sather	Reg. No. <u>44,316</u>
Michelle M. Stempien	Reg. No. <u>41,327</u>
David G. Streeter	Reg. No. <u>43,168</u>
Stephen Todd	Reg. No. <u>47,139</u>
P. Ben Wang	Reg. No. <u>41,420</u>

respectively and individually, as my patent attorneys and/or agents, with full power of substitution and revocation, to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith. Please address all communications to:

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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

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Signature:



Date:

Sept. 10, 2001

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Residence:

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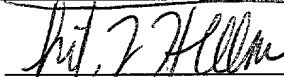
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Signature:



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4W

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5W

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660

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810

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2001-09-13 10:00:00

SEQUENCE LISTING

<110> INCYTE GENOMICS, INC.

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BANDMAN, Olga
YUE, Henry
BAUGHN, Mariah R.
LAL, Preeti
LU, Dyung Aina M.
SHAH, Purvi
AZIMZAI, Yalda

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Glu	His	Ala	Tyr											

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 Cys Leu Glu Gly Leu Val Arg Gly Leu Gln Val Phe Lys Glu Arg
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 Gln Lys Leu Ile Ile Thr Glu Glu Thr Ala Lys Ile Arg Pro Phe
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 Thr Gly Thr Asp Phe Thr Lys Ala Lys Ile Val Leu Asp Ile Ile
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Thr Thr Gln Pro Val	Glu Asp Glu Arg	Gly Asn Val Phe Leu	Trp
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Asn Gly Glu Ile Phe	Ser Gly Ile Lys	Val Glu Ala Glu Glu	Asn
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Asp Thr Gln Ile Leu	Phe Asn Tyr Leu	Ser Ser Cys Lys Asn	Glu
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Ser Glu Ile Leu Ser	Leu Phe Ser Glu	Val Gln Gly Pro Trp	Ser
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 Ile Asp Leu Lys Ser Thr Val Ile Ser Arg Cys Ile Ile Leu Gln
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 Val Ser Val Val Ala Asn Glu Ala Lys Leu Tyr Leu Glu Lys Pro
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 Pro Ser Arg Ile Trp Asn Phe Val Glu Ile Asn Val Ser Met Glu
 425 430 435
 Glu Leu Gln Lys Leu Arg Arg Thr Arg Ile Cys His Leu Ile Arg
 440 445 450
 Pro Leu Asp Thr Val Leu Asp Asp Ser Ile Gly Cys Ala Val Trp
 455 460 465
 Phe Ala Ser Arg Gly Ile Gly Trp Leu Val Ala Gln Glu Gly Val
 470 475 480
 Lys Ser Tyr Gln Ser Asn Ala Lys Val Val Leu Thr Gly Ile Gly
 485 490 495
 Ala Asp Glu Gln Leu Ala Gly Tyr Ser Arg His Arg Val Arg Phe
 500 505 510
 Gln Ser His Gly Leu Glu Gly Leu Asn Lys Glu Ile Met Met Glu
 515 520 525
 Leu Gly Arg Ile Ser Ser Arg Asn Leu Gly Arg Asp Asp Arg Val
 530 535 540
 Ile Gly Asp His Gly Lys Glu Ala Arg Phe Pro Phe Leu Asp Glu
 545 550 555
 Asn Val Val Ser Phe Leu Asn Ser Leu Pro Ile Trp Glu Lys Ala
 560 565 570
 Asn Leu Thr Leu Pro Arg Gly Ile Gly Glu Lys Leu Leu Leu Arg
 575 580 585
 Leu Ala Ala Val Glu Leu Gly Leu Thr Ala Ser Ala Leu Leu Pro
 590 595 600
 Lys Arg Ala Met Gln Phe Gly Ser Arg Ile Ala Lys Met Glu Lys

Ile Asn Glu Lys	605	Ser Asp Lys Cys	610	Gly Arg Leu Gln Ile	615
	620		625		630
Ser Leu Glu Asn Leu	635	Ser Ile Glu Lys	640	Glu Thr Lys Leu	

<210> 6

<211> 660

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2579405CD1

<400> 6

Met Asp Ile Leu Val	5	Ser Glu Cys Ser	10	Ala Arg Leu Leu Gln Gln	15
	20		25		30
Glu Glu Glu Ile Lys	35	Ser Leu Thr Ala	40	Glu Ile Asp Arg Leu Lys	45
	50		55		60
Asn Cys Gly Cys Leu	65	Gly Ala Ser Pro	70	Asn Leu Glu Gln Leu Gln	75
	80		85		90
Glu Glu Asn Leu Lys	95	Leu Lys Tyr Arg	100	Leu Asn Ile Leu Arg Lys	105
	110		115		120
Ser Leu Gln Ala Glu	125	Arg Asn Lys Pro	130	Thr Lys Asn Met Ile Asn	135
	140		145		150
Ile Ile Ser Arg Leu	155	Gln Glu Val Phe	160	Gly His Ala Ile Lys Ala	165
	170		175		180
Ala Tyr Pro Asp Phe	185	Glu Asn Pro Pro	190	Leu Leu Val Thr Pro Ser	195
	200		205		210
Gln Gln Ala Lys Phe	215	Gly Asp Tyr Gln	220	Cys Asn Ser Ala Met Gly	225
	230		235		240
Ile Ser Gln Met Leu	245	Lys Thr Lys Glu	250	Gln Lys Val Asn Pro Arg	255
	260		265		270
Glu Ile Ala Glu Asn	275	Ile Thr Lys His	280	Leu Pro Asp Asn Glu Cys	285
	290		295		300
Ile Glu Lys Val Glu	305	Ile Ala Gly Pro	310	Gly Phe Ile Asn Val His	315
	320		325		330
Leu Arg Lys Asp Phe	335	Val Ser Glu Gln	340	Leu Thr Ser Leu Leu Val	345
	350		355		360
Asn Gly Val Gln Leu	365	Pro Ala Leu Gly	370	Glu Asn Lys Lys Val Ile	375
Val Asp Phe Ser Ser		Pro Asn Ile Ala		Lys Glu Met His Val Gly	
His Leu Arg Ser Thr		Ile Ile Gly Glu		Ser Ile Ser Arg Leu Phe	
Glu Phe Ala Gly Tyr		Asp Val Leu Arg		Leu Asn His Val Gly Asp	
Trp Gly Thr Gln Phe		Gly Met Leu Ile		Ala His Leu Gln Asp Lys	
Phe Pro Asp Tyr Leu		Thr Val Ser Pro		Pro Ile Gly Asp Leu Gln	
Val Phe Tyr Lys Glu		Ser Lys Lys Arg		Phe Asp Thr Glu Glu Glu	
Phe Lys Lys Arg Ala		Tyr Gln Cys Val		Val Leu Leu Gln Gly Lys	
Asn Pro Asp Ile Thr		Lys Ala Trp Lys		Leu Ile Cys Asp Val Ser	
Arg Gln Glu Leu Asn		Lys Ile Tyr Asp		Ala Leu Asp Val Ser Leu	
Ile Glu Arg Gly Glu		Ser Phe Tyr Gln		Asp Arg Met Asn Asp Ile	
Val Lys Glu Phe Glu		Asp Arg Gly Phe		Val Gln Val Asp Asp Gly	
Arg Lys Ile Val Phe		Val Pro Gly Cys		Ser Ile Pro Leu Thr Ile	

Val Lys Ser Asp Gly Gly Tyr Thr Tyr Asp Thr Ser Asp Leu Ala
 380 385 390
 Ala Ile Lys Gln Arg Leu Phe Glu Glu Lys Ala Asp Met Ile Ile
 395 400 405
 Tyr Val Val Asp Asn Gly Gln Ser Val His Phe Gln Thr Ile Phe
 410 415 420
 Ala Ala Ala Gln Met Ile Gly Trp Tyr Asp Pro Lys Val Thr Arg
 425 430 435
 Val Phe His Ala Gly Phe Gly Val Val Leu Gly Glu Asp Lys Lys
 440 445 450
 Lys Phe Lys Thr Arg Ser Gly Glu Thr Val Arg Leu Met Asp Leu
 455 460 465
 Leu Gly Glu Gly Leu Lys Arg Ser Met Asp Lys Leu Lys Glu Lys
 470 475 480
 Glu Arg Asp Lys Val Leu Thr Ala Glu Glu Leu Asn Ala Ala Gln
 485 490 495
 Thr Ser Val Ala Tyr Gly Cys Ile Lys Tyr Ala Asp Leu Ser His
 500 505 510
 Asn Arg Leu Asn Asp Tyr Ile Phe Ser Phe Asp Lys Met Leu Asp
 515 520 525
 Asp Arg Gly Asn Thr Ala Ala Tyr Leu Leu Tyr Ala Phe Thr Arg
 530 535 540
 Ile Arg Ser Ile Ala Arg Leu Ala Asn Ile Asp Glu Glu Met Leu
 545 550 555
 Gln Lys Ala Ala Arg Glu Thr Lys Ile Leu Leu Asp His Glu Lys
 560 565 570
 Glu Trp Lys Leu Gly Arg Cys Ile Leu Arg Phe Pro Glu Ile Leu
 575 580 585
 Gln Lys Ile Leu Asp Leu Phe Leu His Thr Leu Cys Asp Tyr
 590 595 600
 Ile Tyr Glu Leu Ala Thr Ala Phe Thr Glu Phe Tyr Asp Ser Cys
 605 610 615
 Tyr Cys Val Glu Lys Asp Arg Gln Thr Gly Lys Ile Leu Lys Val
 620 625 630
 Asn Met Trp Arg Met Leu Leu Cys Glu Ala Val Ala Ala Val Met
 635 640 645
 Ala Lys Gly Phe Asp Ile Leu Gly Ile Lys Pro Val Gln Arg Met
 650 655 660

<210> 7
 <211> 725
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2662427CD1

<400> 7
 Met Ala Ala Ala Ser Ala Val Ser Val Leu Leu Val Ala Ala Glu
 1 5 10 15
 Arg Asn Arg Trp His Arg Leu Pro Ser Leu Leu Leu Pro Pro Arg
 20 25 30
 Thr Trp Val Trp Arg Gln Arg Thr Met Lys Tyr Thr Thr Ala Thr
 35 40 45
 Gly Arg Asn Ile Thr Lys Val Leu Ile Ala Asn Arg Gly Glu Ile
 50 55 60
 Ala Cys Arg Val Met Arg Thr Ala Lys Lys Leu Gly Val Gln Thr
 65 70 75
 Val Ala Val Tyr Ser Glu Ala Asp Arg Asn Ser Met His Val Asp
 80 85 90
 Met Ala Asp Glu Ala Tyr Ser Ile Gly Pro Ala Pro Ser Gln Gln
 95 100 105
 Ser Tyr Leu Ser Met Glu Lys Ile Ile Gln Val Ala Lys Thr Ser
 110 115 120

Ala Ala Gln Ala Ile His Pro Gly Cys Arg Phe Leu Ser Glu Asn
 125 130 135
 Met Glu Phe Ala Glu Leu Cys Lys Gln Glu Gly Ile Ile Phe Ile
 140 145 150
 Gly Pro Pro Pro Ser Ala Ile Arg Asp Met Gly Ile Lys Ser Thr
 155 160 165
 Ser Lys Ser Ile Met Ala Ala Ala Gly Val Pro Val Val Glu Gly
 170 175 180
 Tyr His Gly Glu Asp Gln Ser Asp Gln Cys Leu Lys Glu His Ala
 185 190 195
 Arg Arg Ile Gly Tyr Pro Val Met Ile Lys Ala Val Arg Gly Gly
 200 205 210
 Gly Gly Lys Gly Met Arg Ile Val Arg Ser Glu Gln Glu Phe Gln
 215 220 225
 Glu Gln Leu Glu Ser Ala Arg Arg Glu Ala Lys Lys Ser Phe Asn
 230 235 240
 Asp Asp Ala Met Leu Ile Glu Lys Phe Val Asp Thr Pro Arg His
 245 250 255
 Val Glu Val Gln Val Phe Gly Asp His His Gly Asn Ala Val Tyr
 260 265 270
 Leu Phe Glu Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile
 275 280 285
 Ile Glu Glu Ala Pro Ala Pro Gly Ile Lys Ser Glu Val Arg Lys
 290 295 300
 Lys Leu Gly Glu Ala Ala Val Arg Ala Ala Lys Ala Val Asn Tyr
 305 310 315
 Val Gly Ala Gly Thr Val Glu Phe Ile Met Asp Ser Lys His Asn
 320 325 330
 Phe Cys Phe Met Glu Met Asn Thr Arg Leu Gln Val Glu His Pro
 335 340 345
 Val Thr Glu Met Ile Thr Gly Thr Asp Leu Val Glu Trp Gln Leu
 350 355 360
 Arg Ile Ala Ala Gly Glu Lys Ile Pro Leu Ser Gln Glu Glu Ile
 365 370 375
 Thr Leu Gln Gly His Ala Phe Glu Ala Arg Ile Tyr Ala Glu Asp
 380 385 390
 Pro Ser Asn Asn Phe Met Pro Val Ala Gly Pro Leu Val His Leu
 395 400 405
 Ser Thr Pro Arg Ala Asp Pro Ser Thr Arg Ile Glu Thr Gly Val
 410 415 420
 Arg Gln Gly Asp Glu Val Ser Val His Tyr Asp Pro Met Ile Ala
 425 430 435
 Lys Leu Val Val Trp Ala Ala Asp Arg Gln Ala Ala Leu Thr Lys
 440 445 450
 Leu Arg Tyr Ser Leu Arg Gln Tyr Asn Ile Val Gly Leu Pro Thr
 455 460 465
 Asn Ile Asp Phe Leu Leu Asn Leu Ser Gly His Pro Glu Phe Glu
 470 475 480
 Ala Gly Asn Val His Thr Asp Phe Ile Pro Gln His His Lys Gln
 485 490 495
 Leu Leu Leu Ser Arg Lys Ala Ala Ala Lys Glu Ser Leu Cys Gln
 500 505 510
 Ala Ala Leu Gly Leu Ile Leu Lys Glu Lys Ala Met Thr Asp Thr
 515 520 525
 Phe Thr Leu Gln Ala His Asp Gln Phe Ser Pro Phe Ser Ser Ser
 530 535 540
 Ser Gly Arg Arg Leu Asn Ile Ser Tyr Thr Arg Asn Met Thr Leu
 545 550 555
 Lys Asp Gly Lys Asn Asn Val Ala Ile Ala Val Thr Tyr Asn His
 560 565 570
 Asp Gly Ser Tyr Ser Met Gln Ile Glu Asp Lys Thr Phe Gln Val
 575 580 585
 Leu Gly Asn Leu Tyr Ser Glu Gly Asp Cys Thr Tyr Leu Lys Cys
 590 595 600
 Ser Val Asn Gly Val Ala Ser Lys Ala Lys Leu Ile Ile Leu Glu

Asn Thr Ile Tyr	605	610	615
Leu Phe Ser Lys Glu	620	Gly Ser Ile Glu Ile Asp	630
Ile Pro Val Pro	635	640	645
Lys Tyr Leu Ser Ser	650	Val Ser Ser Gln Glu Thr	660
Gln Gly Gly Pro	665	670	675
Leu Ala Pro Met Thr	680	Gly Thr Ile Glu Lys Val	690
Phe Val Lys Ala	695	600	705
Gly Asp Lys Val Lys	710	Ala Gly Asp Ser Leu Met	720
Val Met Ile Ala	725	Thr Ile Lys Ser Pro Lys	
Asp Gly Thr Val		Lys Val Phe Tyr Arg Glu Gly Ala Gln Ala	
Asn Arg His Thr		Pro Leu Val Glu Phe Glu Glu Glu Glu Ser Asp	
Lys Arg Glu Ser			

<210> 8

<211> 644

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2844928CD1

<400> 8

Met Ala Val Tyr Val	5	Gly Met Leu Arg Leu	10	Gly Arg Leu Cys Ala	15
Gly Ser Ser Gly Val	20	Leu Gly Ala Arg Ala	25	Ala Leu Ser Arg Ser	30
Trp Gln Glu Ala Arg	35	Leu Gln Gly Val Arg	40	Phe Leu Ser Ser Arg	45
Glu Val Asp Arg Met	50	Val Ser Thr Pro Ile	55	Gly Gly Leu Ser Tyr	60
Val Gln Gly Cys Thr	65	Lys Lys His Leu Asn	70	Ser Lys Thr Val Gly	75
Gln Cys Leu Glu Thr	80	Thr Ala Gln Arg Val	85	Pro Glu Arg Glu Ala	90
Leu Val Val Leu His	95	Glu Asp Val Arg Leu	100	Thr Phe Ala Gln Leu	105
Lys Glu Glu Val Asp	110	Lys Ala Ala Ser Gly	115	Leu Leu Ser Ile Gly	120
Leu Cys Lys Gly Asp	125	Arg Leu Gly Met Trp	130	Gly Pro Asn Ser Tyr	135
Ala Trp Val Leu Met	140	Gln Leu Ala Thr Ala	145	Gln Ala Gly Ile Ile	150
Leu Val Ser Val Asn	155	Pro Ala Tyr Gln Ala	160	Met Glu Leu Glu Tyr	165
Val Leu Lys Lys Val	170	Gly Cys Lys Ala Leu	175	Val Phe Pro Lys Gln	180
Phe Lys Thr Gln Gln	185	Tyr Tyr Asn Val Leu	190	Lys Gln Ile Cys Pro	195
Glu Val Glu Asn Ala	200	Gln Pro Gly Ala Leu	205	Lys Ser Gln Arg Leu	210
Pro Asp Leu Thr Thr	215	Val Ile Ser Val Asp	220	Ala Pro Leu Pro Gly	225
Thr Leu Leu Leu Asp	230	Glu Val Val Ala Ala	235	Gly Ser Thr Arg Gln	240
His Leu Asp Gln Leu	245	Gln Tyr Asn Gln Gln	250	Phe Leu Ser Cys His	255
Asp Pro Ile Asn Ile	260	Gln Phe Thr Ser Gly	265	Thr Thr Gly Ser Pro	270
Lys Gly Ala Thr Leu	275	Ser His Tyr Asn Ile	280	Val Asn Asn Ser Asn	285

Ile Leu Gly Glu Arg Leu Lys Leu His Glu Lys Thr Pro Glu Gln
 290 300
 Leu Arg Met Ile Leu Pro Asn Pro Leu Tyr His Cys Leu Gly Ser
 305 315
 Val Ala Gly Thr Met Met Cys Leu Met Tyr Gly Ala Thr Leu Ile
 320 330
 Leu Ala Ser Pro Ile Phe Asn Gly Lys Lys Ala Leu Glu Ala Ile
 335 345
 Ser Arg Glu Arg Gly Thr Phe Leu Tyr Gly Thr Pro Thr Met Phe
 350 360
 Val Asp Ile Leu Asn Gln Pro Asp Phe Ser Ser Tyr Asp Ile Ser
 365 375
 Thr Met Cys Gly Gly Val Ile Ala Gly Ser Pro Ala Pro Pro Glu
 380 390
 Leu Ile Arg Ala Ile Ile Asn Lys Ile Asn Met Lys Asp Leu Val
 395 405
 Val Ala Tyr Gly Thr Thr Glu Asn Ser Pro Val Thr Phe Ala His
 410 420
 Phe Pro Glu Asp Thr Val Glu Gln Lys Ala Glu Ser Val Gly Arg
 425 435
 Ile Met Pro His Thr Glu Ala Arg Ile Met Asn Met Glu Ala Gly
 440 450
 Thr Leu Ala Lys Leu Asn Thr Pro Gly Glu Leu Cys Ile Arg Gly
 455 465
 Tyr Cys Val Met Leu Gly Tyr Trp Gly Glu Pro Gln Lys Thr Glu
 470 480
 Glu Ala Val Asp Gln Asp Lys Trp Tyr Trp Thr Gly Asp Val Ala
 485 495
 Thr Met Asn Glu Gln Gly Phe Cys Lys Ile Val Gly Arg Ser Lys
 500 510
 Asp Met Ile Ile Arg Gly Gly Glu Asn Ile Tyr Pro Ala Glu Leu
 515 525
 Glu Asp Phe Phe His Thr His Pro Lys Val Gln Glu Val Gln Val
 530 540
 Arg His Leu Ala Gln Val Ser Pro Gln Lys Gln Glu Thr His Met
 545 555
 Asn Thr Val Met Ser Asp Ile Phe Leu Trp Pro Trp Asn Val Val
 560 570
 Gly Val Lys Asp Asp Arg Met Gly Glu Glu Ile Cys Ala Cys Ile
 575 585
 Arg Leu Lys Asp Gly Glu Glu Thr Thr Val Glu Glu Ile Lys Ala
 590 600
 Phe Cys Lys Gly Lys Ile Ser His Phe Lys Ile Pro Lys Tyr Ile
 605 615
 Val Phe Val Thr Asn Tyr Pro Leu Thr Ile Ser Gly Lys Ile Gln
 620 630
 Lys Phe Lys Leu Arg Glu Gln Met Glu Arg His Leu Asn Leu
 635 640

<210> 9

<211> 504

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3231586CD1

<400> 9

Met Phe Pro Arg Glu Lys Thr Trp Asn Ile Ser Phe Ala Gly Cys
 1 5 10 15
 Gly Phe Leu Gly Val Tyr Tyr Val Gly Val Ala Ser Cys Leu Arg
 20 25 30
 Glu His Ala Pro Phe Leu Val Ala Asn Ala Thr His Ile Tyr Gly
 35 40 45
 Ala Ser Ala Gly Ala Leu Thr Ala Thr Ala Leu Val Thr Gly Val

50 55 60
 Cys Leu Gly Glu Ala Gly Ala Lys Phe Ile Glu Val Ser Lys Glu
 65 70 75
 Ala Arg Lys Arg Phe Leu Gly Pro Leu His Pro Ser Phe Asn Leu
 80 85 90
 Val Lys Ile Ile Arg Ser Phe Leu Leu Lys Val Leu Pro Ala Asp
 95 100 105
 Ser His Glu His Ala Ser Gly Arg Leu Gly Ile Ser Leu Thr Arg
 110 115 120
 Val Ser Asp Gly Glu Asn Val Ile Ile Ser His Phe Asn Ser Lys
 125 130 135
 Asp Glu Leu Ile Gln Ala Asn Val Cys Ser Gly Phe Ile Pro Val
 140 145 150
 Tyr Cys Gly Leu Ile Pro Pro Ser Leu Gln Gly Val Arg Tyr Val
 155 160 165
 Asp Gly Gly Ile Ser Asp Asn Leu Pro Leu Tyr Glu Leu Lys Asn
 170 175 180
 Thr Ile Thr Val Ser Pro Phe Ser Gly Glu Ser Asp Ile Cys Pro
 185 190 195
 Gln Asp Ser Ser Thr Asn Ile His Glu Leu Arg Val Thr Asn Thr
 200 205 210
 Ser Ile Gln Phe Asn Leu Arg Asn Leu Tyr Arg Leu Ser Lys Ala
 215 220 225
 Leu Phe Pro Pro Glu Pro Leu Val Leu Arg Glu Met Cys Lys Gln
 230 235 240
 Gly Tyr Arg Asp Gly Leu Arg Phe Leu Gln Arg Asn Gly Leu Leu
 245 250 255
 Asn Arg Pro Asn Pro Leu Leu Ala Leu Pro Pro Ala Arg Pro His
 260 265 270
 Gly Pro Glu Asp Lys Asp Gln Ala Val Glu Ser Ala Gln Ala Glu
 275 280 285
 Asp Tyr Ser Gln Leu Pro Gly Glu Asp His Ile Leu Glu His Leu
 290 295 300
 Pro Ala Arg Leu Asn Glu Ala Leu Leu Glu Ala Cys Val Glu Pro
 305 310 315
 Thr Asp Leu Leu Thr Thr Leu Ser Asn Met Leu Pro Val Arg Leu
 320 325 330
 Ala Thr Ala Met Met Val Pro Tyr Thr Leu Pro Leu Glu Ser Ala
 335 340 345
 Leu Ser Phe Thr Ile Arg Leu Leu Glu Trp Leu Pro Asp Val Pro
 350 355 360
 Glu Asp Ile Arg Trp Met Lys Glu Gln Thr Gly Ser Ile Cys Gln
 365 370 375
 Tyr Leu Val Met Arg Ala Lys Arg Lys Leu Gly Arg His Leu Pro
 380 385 390
 Ser Arg Leu Pro Glu Gln Val Glu Leu Arg Arg Val Gln Ser Leu
 395 400 405
 Pro Ser Val Pro Leu Ser Cys Ala Ala Tyr Arg Glu Ala Leu Pro
 410 415 420
 Gly Trp Met Arg Asn Asn Leu Ser Leu Gly Asp Ala Leu Ala Lys
 425 430 435
 Trp Glu Glu Cys Gln Arg Gln Leu Leu Leu Gly Leu Phe Cys Thr
 440 445 450
 Asn Val Ala Phe Pro Pro Glu Ala Leu Arg Met Arg Ala Pro Ala
 455 460 465
 Asp Pro Ala Pro Ala Pro Ala Asp Pro Ala Ser Pro Gln His Gln
 470 475 480
 Leu Ala Gly Pro Ala Pro Leu Leu Ser Thr Pro Ala Pro Glu Ala
 485 490 495
 Arg Pro Val Ile Gly Ala Leu Gly Leu
 500
 <210> 10
 <211> 489
 <212> PRT
 <213> Homo sapiens

<223> Incyte ID No: 3580770CD1

Met	Lys	Tyr	Ile	Leu	Val	Thr	Gly	Gly	Val	Ile	Ser	Gly	Ile	Gly
1				5					10					15
Lys	Gly	Ile	Ile	Ala	Ser	Ser	Ile	Gly	Thr	Ile	Leu	Lys	Ser	Cys
				20					25					30
Gly	Leu	Arg	Val	Thr	Ala	Ile	Lys	Ile	Asp	Pro	Tyr	Ile	Asn	Ile
				35					40					45
Asp	Ala	Gly	Thr	Phe	Ser	Pro	Tyr	Glu	His	Gly	Glu	Val	Phe	Val
				50					55					60
Leu	Asn	Asp	Gly	Gly	Glu	Val	Asp	Leu	Asp	Leu	Gly	Asp	Tyr	Glu
				65					70					75
Arg	Phe	Leu	Asp	Ile	Asn	Leu	Tyr	Lys	Asp	Thr	Ile	Val	Thr	Thr
				80					85					90
Gly	Lys	Ile	Tyr	Gln	His	Val	Ile	Asn	Lys	Glu	Arg	Arg	Gly	Asp
				95					100					105
Tyr	Leu	Gly	Lys	Thr	Val	Gln	Val	Val	Pro	His	Ile	Thr	Asp	Ala
				110					115					120
Val	Gln	Glu	Trp	Val	Met	Asn	Gln	Ala	Lys	Val	Pro	Val	Asp	Gly
				125					130					135
Asn	Lys	Glu	Glu	Pro	Gln	Ile	Cys	Val	Ile	Glu	Leu	Gly	Gly	Thr
				140					145					150
Ile	Gly	Asp	Ile	Glu	Gly	Met	Pro	Phe	Val	Glu	Ala	Phe	Arg	Gln
				155					160					165
Phe	Gln	Phe	Lys	Ala	Lys	Arg	Glu	Asn	Phe	Cys	Asn	Ile	His	Val
				170					175					180
Ser	Leu	Val	Pro	Gln	Leu	Ser	Ala	Thr	Gly	Glu	Gln	Lys	Thr	Lys
				185					190					195
Pro	Thr	Gln	Asn	Ser	Val	Arg	Ala	Leu	Arg	Gly	Leu	Gly	Leu	Ser
				200					205					210
Pro	Asp	Leu	Ile	Val	Cys	Arg	Ser	Ser	Thr	Pro	Ile	Glu	Met	Ala
				215					220					225
Val	Lys	Glu	Lys	Ile	Ser	Met	Phe	Cys	His	Val	Asn	Pro	Glu	Gln
				230					235					240
Val	Ile	Cys	Ile	His	Asp	Val	Ser	Ser	Thr	Tyr	Arg	Val	Pro	Val
				245					250					255
Leu	Leu	Glu	Glu	Gln	Ser	Ile	Val	Lys	Tyr	Phe	Lys	Glu	Arg	Leu
				260					265					270
His	Leu	Pro	Ile	Gly	Asp	Ser	Ala	Ser	Asn	Leu	Leu	Phe	Lys	Trp
				275					280					285
Arg	Asn	Met	Ala	Asp	Arg	Tyr	Glu	Arg	Leu	Gln	Lys	Ile	Cys	Ser
				290					295					300
Ile	Ala	Leu	Val	Gly	Lys	Tyr	Thr	Lys	Leu	Arg	Asp	Cys	Tyr	Ala
				305					310					315
Ser	Val	Phe	Lys	Ala	Leu	Glu	His	Ser	Ala	Leu	Ala	Ile	Asn	His
				320					325					330
Lys	Leu	Asn	Leu	Met	Val	Ile	Asp	Met	Pro	Glu	His	Asn	Pro	Gly
		</												

[illegible]

Thr Gly Asn Leu Asn Ala Tyr Leu Gln Gln Gly Cys Lys Leu Ser
 455 460 465
 Ser Ser Asp Arg Tyr Ser Asp Ala Ser Asp Ser Phe Ser Glu
 470 475 480
 Pro Arg Ile Ala Glu Leu Glu Ile Ser
 485

<210> 11
 <211> 258
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 3778612CD1

<400> 11
 Met Glu Arg Gln Lys Arg Lys Ala Asp Ile Glu Lys Gly Leu Gln
 1 5 10 15
 Phe Ile Gln Ser Thr Leu Pro Leu Lys Gln Glu Glu Tyr Glu Ala
 20 25 30
 Phe Leu Leu Lys Leu Val Gln Asn Leu Phe Ala Glu Gly Asn Asp
 35 40 45
 Leu Phe Arg Glu Lys Asp Tyr Lys Gln Ala Leu Val Gln Tyr Met
 50 55 60
 Glu Gly Leu Asn Val Ala Asp Tyr Ala Ala Ser Asp Gln Val Ala
 65 70 75
 Leu Pro Arg Glu Leu Leu Cys Lys Leu His Val Asn Arg Ala Ala
 80 85 90
 Cys Tyr Phe Thr Met Gly Leu Tyr Glu Lys Ala Leu Glu Asp Ser
 95 100 105
 Glu Lys Ala Leu Gly Pro Asp Ser Glu Ser Ile Arg Ala Leu Phe
 110 115 120
 Arg Lys Ala Arg Ala Leu Asn Glu Leu Gly Arg His Lys Glu Ala
 125 130 135
 Tyr Glu Cys Ser Ser Arg Cys Ser Leu Ala Leu Pro His Asp Glu
 140 145 150
 Ser Val Thr Gln Leu Gly Gln Gly Pro Leu Gly Ser Gly Ala Ser
 155 160 165
 Trp Pro Gly Gln Ser Trp Ser Pro His Arg Val Arg Lys Arg Glu
 170 175 180
 Trp Glu Ala Glu Cys Asp Gly Glu Glu Gly Gln Glu Asp Pro Phe
 185 190 195
 Asn Asp Glu Gly Asn Tyr Phe Ser Cys Glu Pro Ser Arg Ala Pro
 200 205 210
 Gly Trp Glu Ala Gln Arg Thr Glu Ser Gly Thr Cys Val Pro Pro
 215 220 225
 Gly Arg Gln Gly Gln Asp Gly Met Ala Ser Met Gly Ala Gly Trp
 230 235 240
 Val Gly Arg Asp Ala Ala Phe Leu Ser Trp Ala Val Ile Asn Leu
 245 250 255
 Met Val Leu

<210> 12
 <211> 555
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 4574912CD1

<220>
 <221> unsure
 <222> 63-65
 <223> unknown or other

Met	Glu	Gly	Ala	Val	Leu	Glu	Ala	Gly	Gly	Ala	Arg	Cys	Phe	Cys
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Arg	Phe	Gly	Cys	Glu	Leu	Ser	Lys	Tyr	Glu	Asn	Pro	Gly	Tyr	Ser
				20					25					30
Ser	Pro	Arg	Ser	Asp	Tyr	Phe	Lys	Asn	Tyr	Met	Ile	Ile	Ile	Thr
				35					40					45
Gln	Asn	Arg	Met	Ser	Phe	Leu	Ala	Asn	Met	Phe	His	Thr	Met	Asp
				50					55					60
Cys	Val	Xaa	Xaa	Xaa	Arg	Tyr	Ser	Cys	Gly	Pro	Thr	Val	Tyr	Asp
				65					70					75
His	Ala	His	Leu	Gly	His	Ala	Cys	Ser	Tyr	Val	Arg	Phe	Asp	Ile
				80					85					90
Ile	Arg	Arg	Ile	Leu	Thr	Lys	Val	Phe	Gly	Cys	Ser	Ile	Val	Met
				95					100					105
Val	Met	Gly	Ile	Thr	Asp	Val	Asp	Asp	Lys	Ile	Ile	Lys	Arg	Ala
				110					115					120
Asn	Glu	Met	Asn	Ile	Ser	Pro	Ala	Ser	Leu	Ala	Ser	Leu	Tyr	Glu
				125					130					135
Glu	Asp	Phe	Lys	Gln	Asp	Met	Ala	Ala	Leu	Lys	Val	Leu	Pro	Pro
				140					145					150
Thr	Val	Tyr	Leu	Arg	Val	Thr	Glu	Asn	Ile	Pro	Gln	Ile	Ile	Ser
				155					160					165
Phe	Ile	Glu	Gly	Ile	Ile	Ala	Arg	Gly	Asn	Ala	Tyr	Ser	Thr	Ala
				170					175					180
Lys	Gly	Asn	Val	Tyr	Phe	Asp	Leu	Lys	Ser	Arg	Gly	Asp	Lys	Tyr
				185					190					195
Gly	Lys	Leu	Val	Gly	Val	Val	Pro	Gly	Pro	Val	Gly	Glu	Pro	Ala
				200					205					210
Asp	Ser	Asp	Lys	Arg	His	Ala	Ser	Asp	Phe	Ala	Leu	Trp	Lys	Ala
				215					220					225
Ala	Lys	Pro	Gln	Glu	Val	Phe	Trp	Ala	Ser	Pro	Trp	Gly	Pro	Gly
				230					235					240
Arg	Pro	Gly	Trp	His	Ile	Glu	Cys	Ser	Ala	Ile	Ala	Ser	Met	Val
				245					250					255
Phe	Gly	Ser	Gln	Leu	Asp	Ile	His	Ser	Gly	Gly	Ile	Asp	Leu	Ala
				260					265					270
Phe	Pro	His	His	Glu	Asn	Glu	Ile	Ala	Gln	Cys	Glu	Val	Phe	His
				275					280					285
Gln	Cys	Glu	Gln	Trp	Gly	Asn	Tyr	Phe	Leu	His	Ser	Gly	His	Leu
				290					295					300
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Phe	Arg	Phe	Phe	Cys	Leu	Arg	Ser	Ser	Tyr	Arg	Ser	Ala	Ile	Asp
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 Ala Asp Ser Gly Leu Lys Ile Leu Ala Cys Asp Asp Leu Asp Glu
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<213> Homo sapiens

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<221> misc_feature

<223> Incyte ID No: 5854855CD1

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Gly Arg Leu Leu Leu	Arg Val Leu His	Val Ser Glu Asn Pro	Val
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Pro Leu Thr Val Arg	Val Ser Pro Glu	Val Arg Asp Val Arg	Pro
	80	85	90
Tyr Ile Val Gly Ala	Val Val Arg Gly	Met Asp Leu Gln Pro	Gly
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Asn Ala Leu Lys Arg	Phe Leu Thr Ser	Gln Thr Lys Leu His	Glu
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Asp Leu Cys Glu Lys	Arg Thr Ala Ala	Thr Leu Ala Thr His	Glu
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Gln Asp Leu Lys Ile	Val Pro Leu Gly	Arg Lys Glu Ala Lys	Ala
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Lys Glu Leu Val Arg	Gln Leu Gln Leu	Glu Ala Glu Glu Gln	Arg
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Lys Gln Lys Lys Arg	Gln Ser Val Ser	Gly Leu His Arg Tyr	Leu
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His Leu Leu Asp Gly	Asn Glu Asn Tyr	Pro Cys Leu Val Asp	Ala
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Asp Gly Asp Val Ile	Ser Phe Pro Pro	Ile Thr Asn Ser Glu	Lys
	215	220	225
Thr Lys Val Lys Lys	Thr Thr Ser Asp	Leu Phe Leu Glu Val	Thr
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	260	265	270
Glu Glu Gly Ser Leu	Ser Asp Thr Glu	Ala Asp Ala Val Ser	Gly
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<212> DNA

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<212> DNA

<213> Homo sapiens

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 <213> Homo sapiens

<220>
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 <213> Homo sapiens

<220>
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 <223> Incyte ID No: 2844928CB1

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 <211> 1954
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> Incyte ID No: 3231586CB1

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<210> 25

<211> 1937

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3580770CB1

<400> 25

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<213> Homo sapiens

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<223> Incyte ID No: 3778612CB1

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<211> 1810

<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 4574912CB1

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<221> unsure

<222> 193, 196-198

<223> a, t, c, g, or other

<400> 27

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